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                                                                                                                          February 27, 2006, 17:55:43; Search time 187 Seconds (without alignments) 472.273 Million cell updates/sec
                                                                                                                                                                                               US-10-696-259-6
1067
1 MAWMLLLILIMVHPGSCALW.....APLPPPCGSSAHLLPPVPGG 201
                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     2443163 seqs, 439378781 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay06403 Human B-c			_	Ado19810 Human PRO	Adq30923 Human NKp	Aay06401 Human B-c	Ξ.		_	_	Aae02771 Human NKp	Human	Human	Human	Aea40197 Peptide (	Aae20273 Human lun	Aar60134 CTLA4 rec	Aar77642 Full leng	Aay43479 Amino aci	Aaw81584 Human CTL	Abb78106 Amino aci	Human	Himan
SUMMARIES	ID	AAY06403	ADY16489	AEA40207	AAE02769	ADO19810	ADQ30923	AAY06401	AAY06402	ADY16598	AAE19109	AAE19110	AAE02771	ADQ30924	ADP48750	AEA40208	AEA40197	AAE20273	AAR60134	AAR77642	AAY43479	AAW81584	ABB78106	AAU75124	AA1175132
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ADPS6715 Human CTL Add89013 CTLA4 rec Ad98950 UTLA4 rec Ad98550 Human CTL Adv98655 Human CTL Adv76124 Protein 8 Adv75127 Human CTL Adv75127 Human CTL Adv75130 Human CTL Adv75131 Human CTL Adv7513 Human CTL Adv7513 Human CTL Adv7513 Human CTL Adv7513 Human CTL Adv751469 Human CTL Adv751469 Human CTL Adv751469 Human CTL		an; y; osis.	nal end"	ALE COPY
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1	ALIG standard; protein; 201 AA. 99 (first entry)	myelin oligodendrocyte (uction; immunomodulator sease; inflammation; ge	Location/Qualifi 112 /note= "leader p 13201 /note= "mature p 42 /note= "N-glycos 68 /note= "N-glycos 121 /note= "N-glycos 139162 /note= "transmem 166201 /note= "alternat	-USO23826.
25 125 125 125 125 125 125 125 125 125 1	06403 stan 06403; 08P-1999	i, B-cell al transd timmune di	7 9 4 4 4 7	W09923867-A2. 20-MAY-1999. 05-NOV-1998; 98WO 07-NOV-1997; 97US (BIOJ ) BIOGEN INC. Browning J; WPI; 1999-418423/35 N-PSDB; AAX59349.
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Mandelboim O,
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                                          This sequence represents human BMOG, a novel member of the B cell myelin obligodemofracyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAYO6401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)
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100.0%; Score 1067; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.2e-93;
Matches 201; Conservative 0; Mismatches 0;
B-cell myelin oligodendrocyte glycoproteins
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                    Claim 2; Page 43; 43pp; English
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                                                                                                                                                                                                polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
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New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus
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                                                                                                                                                                        to an isolated nucleic acid
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// Pred. No. 4.2e-93;
0; Mismatches 0;
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                                                                                                            Claim 8; SEQ ID NO 2295; 158pp; English
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(UYNE ) UNIV BEN-GURION NEGEV
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                                                                                                                                                                     The invention relates
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 201 AA;
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Location/Qualifiers

Homo sapiens.

Peptide

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The invention relates to isolated peptide fragments of a natural cytotoxicity receptor (NCR) of natural killer (NK) cells, or active tragments, analogs or derivatives, wherein the peptide fragment is capable of binding to a membrane-associated biomolecule of a tumor cell, and the biomolecule comprises at least one sulfated polyasccharide, and serves as the binding site of the NCR mediating the lysis of tumor cells by NK cells, with the proviso that the peptide is other than a full ength NCR polypeptide or an isolated NCR extracellular domain. Also described are: (1) an antibody that recognizes an epitope on a target membrane-associated biomolecule of a tumor cell, the biomolecule of cumor cells by NK cells via the NCR; (2) a method of targeting a tumor cells by NK cells via the NCR; (2) a method of targeting a tumor cell shy NK cells via the NCR; (2) a method of targeting a tumor cells by NK cells via the NCR; (2) a method of targeting a tumor cell shy NK cells via the NCR; (2) a method of binding to a membrane-associated sulfated polysaccharide of a tumor cell. The peptide is a fragment of NCR which are capable of binding to a cidantifying peptide is a lragment of NCR selected from NKp46. It is a fragment of the D2 domain of NKp46 comprising a sequence fully defined in the specification (SEQ ID NOS: 1 and 4). Alternatively, the peptide is a fragment of NCR a sequence fully defined in the specification (SEQ ID NOS: 3 and 4). Alternatively, is palected from a sequence fully defined in the specification (SEQ ID NOS: 3 and 4). Alternatively, is can a sequence fully defined in the specification of sequence membrane-associated biomolecule is selected from a sequence fully defined in the specification of SEQ ID NOS: 3 and 4). Alternatively, is can a sequence fully defined in the specification of SEQ ID NOS: 3 and 4). Alternatively, is can also a sequence fully defined in the specification of SEQ ID NOS: 3 and 4). Alternatively of can be shown the specification of NCR and sequence fully defined the specification of NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a proteoglycan. The antibody is capable of blocking the binding of NK cells via NCR to membrane-associated sulfated polysaccharide biomolecules in a cell, therefore, inhibiting NCR-dependent cell lysis associated with autoimmunity. The peptides and antibodies of the invention are useful for targeting a tumor cell in a subject via an NCR-dependent mechanism. The composition and methods of the invention are useful for targeting tumor cells to diagnose and/or treat benign and malignant tumors or proliferative diseases. This sequence represents human natural
Disclosure; SEQ ID NO 13; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytotoxicity receptor, NKp30.
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Sequence 201 AA;

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VPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
                                                                                                                                                    NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGKCLTWKGPRRQLPAVV 180
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Length 201;
                        Indels
100.0%; Score 1067; DB 9; 100.0%; Pred. No. 4.2e-93;
                        Mismatches
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100.0%; FAL
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Human, NKp30 receptor, natural killer cell, cytostatic; antimicrobial, melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour; immunosuppressant; antiviral; drug; grafting enhancement; leukaemia; AAE02769 standard; protein; 190 AA. (first entry) Human NKp30 receptor. 06-AUG-2001 AAE02769; 

therapy

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The invention relates to human NKp30 receptor and its corresponding CDNA molecule which is involved in natural cytotoxicity mediated by natural killer (NK) cells and antibodies that identify the same. NKp30 receptor is a member of immunoglobulin super family (15-SF). NKp30 is selectively expressed on the surface of human mature NK cells. NKp30 and its cDNA are useful for detecting and/or quantifying the presence of NK cells in a biological sample. The invention also provide Kits for detecting and/or quantifying the presence of NK cells, for the selective removal of NK cells from a biological sample, for the positive and selective of NK cells from a biological sample, for the positive and selective of NK cells from a biological sample and for the in vitro cumulation of NK cell cytotoxicity. The invention further provides a pharmaceutical composition which is used as a drug for grafting cellar composition which is used as a drug for grafting versus tumour (GyT) and especially graft versus leukaemia (GyL), and for the prevention, palliation and/or therapy of solid or liquid tumours, cellar and notable and lung adenocarcinoma, and/or continuation of microorganism, notably viral infection. NKp30 antibodies are useful for incroorganism, notably viral infection. 1 MAMMILLILIMYHPGSCALWYSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEV 60 /el compound, useful for detection and/or quantifying the presence of cells, comprises the amino acid sequences of the NKp30 molecule. identifying NKp30 natural ligands and allow assessment of the level of surface NKp30 ligand expressed on an NK-susceptible target cell and the comparison of this level to the standard physiological one. Hence NKp30 antibodies are useful in the diagnosis of tumours or of infection. The 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEV Gaps /label= Extracellular region /note= "Forms an immunoglobulin (Ig) V-like domain" Score 876; DB 4; Length 190; Pred. No. 5.9e-75; 2; Mismatches 7; Indels 12; 19. .190 /label= Mature\_NKp30\_receptor\_protein 'note= "N-glycosylation site" 'note= "N-glycosylation site" 139. .157 /label= Transmembrane\_region /label= Intracellular\_region present sequence is human NKp30 receptor 1. .18 /label= Signal\_peptide Biassoni R; Claim 1; Fig 7B; 83pp; English. L5-NOV-2000; 2000WO-EP011697. 99US-00440514. 82.1%; (INNA-) INNATE PHARMA SAS .138 .190 Conservative Moretta A, Bottino C, WPI; 2001-329221/34. N-PSDB; AAD06564. (UYGE-) UNIV GENOVA. Similarity Sequence 190 AA; WO200136630-A2. Modified-site Modified-site 15-NOV-1999; 15-NOV-1999; 25-MAY-2001. 173; Query Match Local Protein Region Region Region Novel Best Loca Matches 8

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Length 190; Indels 9 9 120 120 172

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|Jabel= Transmembrane region
|/note= "Region specifically described in Claim 3"
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/label= Cytoplasmic tail
/note= "Region specifically described in Claim 3"

    138
    /label= Extracellular region
    /note= "Region specifically described in Claim 3"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.
Score 876; DB 8; Le
Pred. No. 5.9e-75;
                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ30923 standard; protein; 190 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-2003; 2003WO-EP014716.
                     82.1%;
                                      89.28;
                                                                                                                                                                                                                                                                                                                 173 RRQLPAVVPAPLPP 186
                                                                                                                                                                                                                                                                                                                                                  R----GVIPEPRCP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                     Query Match 82.1
Best Local Similarity 89.2
Matches 173; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NKp30 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-507595/48.
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Region
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                                                               Novel PRO polypeptide e.g., PRO69614, PRO711106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, PRO, immune related disorder, systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjosen's syntome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; dentral nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for retaring and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic langule disorders include systemic chronic arthritis, systemic haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or paripheral nervous system, demyelinating diseases of the duillain-Barre syndrome and chronic inflammatory demyelinating polymeuropathy, polyneuropathy. This sequence represents a human PRO polypeptide of the
                                          VPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG
                                                                                                                   ----CLTWKGP
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                                                                                                                     NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; SEQ ID NO 734; 1731pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chiu H,
                                                                                                                                                                                                                                                                                                                         ADO19810 standard; protein; 190 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark H,
                                                                                                                                                                                                                 | | | | | | R----GVIPEPRCP 190
                                                                                                                                                                                          RRQLPAVVPAPLPP 186
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Homo

AD019810;

ADO1981 ID AD RESULT

Fong S, I

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The present sequence is that of human NKp30, a 190 amino acid polypeptide (about 30 kDa on SDS-PAGE) that is selectively expressed by natural
Pharmaceutical compositions that stimulate proliferation of natural killer cells useful for therapy of melanoma, chronic myeloid, and leukemia, comprise an anti-natural killer cell receptor antibody and
                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 1; 35pp; English.
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Sequence 190 AA;

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killer (NK) cells, and particularly by mature NK cells. Claimed pharmaceutical compositions that have a stimulating effect on the proliferation of NK cells comprise an antibody such as an anti-NKp30 antibody or anti-NKp46 antibody or its immuno-reactive fragment and a cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the antibody or its immuno-reactive fragment and incorporate or separately to a subject. The anti-NKp30 antibody is an isolated antibody or its antigen-binding fragment which specifically binds to NKp30 or to a cragment ADQ10924-ADQ30227 of NKp30. The pharmaceutical compositions, when used for daily subcutaneous injection, comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and lower than 1 million units/square meters/day of cytokine(s), are useful for the prevention, cuits/square mid therapy of e.g. melanoma, chronic myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung adenocarcinoma, neuroblastocam and for antimicrobial prevention, palliation and therapy (claimed).
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89.2%; Pred. No. 5.9e-75;
tive 2; Mismatches 7; Indels 12;
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autoimmune disease; inflammation; gene therapy; diagnosis.
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/note= "transmembrane domain"
166. .190
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/note= "leader peptide"
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/note= "mature protein"
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Matches 173; Conservative
                                                                                                                                                                                                                                                                                            Sequence 190 AA;
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This sequence represents human BMOG, a novel member of the B cell myelin oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAYO6401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modularing the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)
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88.7%; Pred. No. 9.1e-75;
ive 3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                        Novel B-cell myelin oligodendrocyte glycoproteins.
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                                                                                                                                                                                                                                                                                           Claim 2; Page 42; 43pp; English.
                                                      98WO-US023826.
                                                                                        97US-0064761P.
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Best Local Similarity 88.7
Matches 172; Conservative
                                                                                                                                                                                                  WPI; 1999-418423/35.
                                                                                                                         (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                      N-PSDB; AAX59347.
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                                                                                        07-NOV-1997;
                                                      05-NOV-1998;
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                 20-MAY-1999,
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05-MAY-2005 (first entry)
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                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                          /note= "alternatively spliced C-terminal end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.5%; Score 859; DB 2; Length 177; 100.0%; Pred. No. 2.2e-73; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel B-cell myelin oligodendrocyte glycoproteins.
                                                                                                                                                           139. .162
/note= "transmembrane domain"
                                                                             note= "N-glycosylated"
                                                                                                                                          'note= "N-glycosylated"
             'note= "leader peptide"
                                             /note= "mature protein"
                                                                                                           'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 43; 43pp; English
                                                                                                                                                                                                                                                                                                                                        97US-0064761P
                                                                                                                                                                                                                                                                                                       98WO-US023826
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N-PSDB; AAX59348.
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                                                                                                                                                                                                                                                                                                                                                                       (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 177 AA;
                                                            Modified-site
                                                                                           Modified-site
                                                                                                                           Wodified-site
                                                                                                                                                                                                                                                                                                          35-NOV-1998;
                                                                                                                                                                                                                                                                                                                                        37-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                        Browning J;
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                            Protein
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ADY16598 standard; protein; 177 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; natural killer cell activating protein; NKp46; therapy; virucide; viral infection; natural killer cell; NK; NKp44; imaging agent; cancer; detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; NKp30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus
                                                        Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive; Antiirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antiabbetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic; Antiallergic; ds; gene; diagnosis.
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100.0%; Pred. No. 2.2e-73;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID NO 2404; 158pp; English.
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PRO polypeptide SEQ ID NO 2404.
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                                                                                                                                                                                                                                                                                                                                                                                                                          11-AUG-2004; 2004WO-US026249.
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Best Local Similarity 100.7
Matches 165, Conservative
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detection of a variety of virtal infections, by using complex agents comprising the natural killer (NK) cells activating proteins, NKp46 and NKp44 and functional fragments thereof, linked to therapeutic or imaging agents. The complex is useful for treating pathologies associated with viral infections (e.g. infections caused by influenza virus, HIV, Epstein -Barr virus, cycomegalovirus, vaccinia virus, ECMV, MWM or herpes virus) and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for the imaging and monitoring of cancer. The complex may also be used to detect the presence of abnormal cells in a sample. The antibodies can be used to qualitatively or quantitatively or quantitatively or quantitatively or grown immunoglobulin (G (IGG)) For region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New targeting complex capable of targeting an active substance to a target cell, comprising a target recognition segment and an active segment, useful for treating pathologies associated with viral infections
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100.0%; Pred. No. 4.3e-59;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 108-110; 113pp; English.
                                                                                                                /note= "Human NKp30"
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE02771 standard; protein; 120 AA.
                                                                                                                                     136. .369
/note= "Human IgG"
                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNE ) UNIV BEN-GURION NEGEV
                                                                                                                                                                                                                                                                                                 19-JUL-2001; 2001WO-IL000664.
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Best Local Similarity 100.7
Matches 135, Conservative
                                                                                          .135
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                                                                                                                                                                                                           WO200208287-A2
Homo sapiens.
                                                                                                                                                                                                                                                        31-JAN-2002.
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                          Chimeric.
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                                                                                             Region
                                                                                                                                        Region
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AAE02771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to compositions and methods for the treatment and detection of a variety of viral infections, by using complex agents comprising the natural killer (NK) cells activating proteins, NKp46 and NKp44 and functional fragments thereof, linked to therapeutic or imaging agents. The complex is useful for treating pathologies associated with viral infections (e.g. infections caused by influenza virus, HIV, Epstein-Barr virus, Cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus) and cancer (e.g. carcinomas, melanomas, lymphomas and sarromas), and for the imaging and monitoring of cancer. The complex may also be used to detect the presence of abnormal cells in a sample. The antibodies can be used to qualitatively or quantitatively detect the ligand for the complex. The present sequence is human NKp30 protein
                                                                                                                                                                                                                                                                                                                                                                                                          New targeting complex capable of targeting an active substance to a target cell, comprising a target recognition segment and an active segment, useful for treating pathologies associated with viral infections
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                                                                                                                                   19-JUL-2001; 2001WO-IL000664.
                                                                                                                                                                                20-JUL-2000; 2000IL-00137419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGTRLVVEKEHPQLG 135
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                                                                                                                                                                                                                                                                                              Mandelboim O, Porgador A;
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Best Local Similarity 100.0
Matches 135, Conservative
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                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD30466.
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                                        WO200208287-A2.
Homo sapiens.
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21-MAY-2002
                                                                                        31-JAN-2002
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Gaps ö

Length 369; 0; Indels

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23-SEP-2004 (first entry)

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molecule which reacted and the corresponding curva molecule which reacted in any receptor and its corresponding curva molecule which is involved in natural cyctoxicity mediated by natural killer (NK) cells and antibodies that identify the same. NKp30 receptor is a member of immunoglobulin super family (Ig-SF). WKp30 and its cDNA are useful for detecting and/or quantifying the presence of NK cells. NKp30 and its cDNA are biological sample. The invention also provide kits for detecting and/or quantifying the presence of NK cells for the selective removal of NK cells from a biological sample, for the positive and selective or purification of NK cells from a biological sample, for the positive and for the in vitro purification of NK cells from a biological sample and for the in vitro seimulation of NK cells from a biological sample and for the in vitro parameterical composition which is used as a drug for grafting chancement, graft versus host (GvH) inhibition, stimulation of graft versus tumour (GvT) and especially graft versus leukaemia (GvT), and for the prevention, palliation and/or therapy of solid or liquid tumours, such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or microorganism, notably viral infection. NKp30 antibodies are useful for comparison of this level to the standard physiological one. Hence NKp30 antibodies are useful in the content of the diagnosis of tumours or of infection. The content of the diagnosis of tumours or of infection. The content of the diagnosis of tumours or of infection. The content of the diagnosis of tumours or of infection. The content of the diagnosis of tumours or of infection. The content of the second or the content of t
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                                               Human, NKp30 receptor; natural killer cell; cytostatic; antimicrobial;
melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to human NKp30 receptor and its corresponding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rel compound, useful for detection and/or quantifying the presence of cells, comprises the amino acid sequences of the NKp30 molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LWVSOPPEIRTLEGSSAFLPCSFNASOGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLA
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100.0%; Pred. No. 5.4e-52;
ive 0; Mismatches 0; Indels
Human NKp30 receptor extracellular region sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blassoni R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1, Fig 7B, 83pp; English.
                                                                                                                                        therapy; extracellular region.
                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00440514
                                                                                                                                                                                                                                                                                                                                                      .S-NOV-2000; 2000WO-EP011697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INNA-) INNATE PHARMA SAS. (UYGE-) UNIV GENOVA.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moretta A, Bottino C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-329221/34
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                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-1999;
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                                                                                                                                                                                             Homo saptens
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The present sequence is that of the extracellular region of human Nkp30 and 20030923, a 190 amino acid polypeptide that is selectively expressed by natural killer. (NK) cells, and particularly by mature NK cells. Claimed plaraceutical compositions that have a stimulating effect on the proliferation of NK cells comprise an antibody such as an anti-NKp30 cutibody or anti-NKp40 antibody or its immuno-reactive fragment and a cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the antibody (ies) and cytokine(s) being administered together or separately cto a subject. The anti-NKp30 antibody is an isolated antibody or its cantibody in the antibody or its antipen-binding fragment which specifically binds to NKp30 or to a fragment, including the extracellular region, of NKp30. The fragment in sto 100 mg/kg (body weight) of antibody (ies), and comprising from 1 ng to 100 mg/kg (body weight) of antibody (ies), and lower than 1 million units/square meters/day of cytokine(s), are useful for the prevention, palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma, heppatocarcinoma, lung adenocarcinoma, neuroblastema and for antimicrobial prevention, palliation and therapy (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
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                                                                                                                                                                                                                                                                                                                                                                                                                              lls useful for therapy of melanoma, chronic myeloid, and comprise an anti-natural killer cell receptor antibody and
                                                                                                                                                                                                                                                                                                                                                                                                            compositions that stimulate proliferation of natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                   Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NKp30-Fc conjugate protein SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 2; 35pp; English.
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                                                Human NKp30 extracellular region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP48750 standard; protein; 382
                                                                                                                                                                                                                                22-DEC-2003; 2003WO-EP014716.
                                                                                                                                                                                                                                                                   23-DEC-2002; 2002US-0435344P
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Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                killer cells useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                         WO2004056392-A1
                                                                                                                                                                                                                                                                                                                                                                                                            Pharmaceutical
                                                                                                                          Homo sapiens.
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ADQ30924;

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polypeptide conjugate; target recognition; natural killer cell receptor; cytostatic; gene therapy; neoplastic disease; tumour; carcinoma; squamous cell carcinoma; adenocarcinoma; small cell carcinoma; melanoma; glioma; neuroblastoma; B cell lymphoma; T cell lymphoma; leukaemia; human; natural killer cytotoxicity receptor conjugate;
                                                                                                                                                                                                                                                                            NKp30-Fc conjugate.
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Homo sapiens

note= "NKp30-Fc conjugate" ocation/Qualifiers . . .25 /label= signal 26. .382 Misc-difference Peptide Protein

16. .31 /note= "KpnI site" 32. .148 /label= NKp30 149. .382 /label= Fc Region Region

WO2004053054-A2

24-JUN-2004.

09-DEC-2003; 2003WO-IL001040.

09-DEC-2002; 2002US-0431728P.

(NATS-) NATSPEARS LTD.

Mandelboim O, Porgador A;

WPI; 2004-468830/44. N-PSDB; ADP48757. New polypeptide conjugate comprising a target recognition segment comprising a Natural Killer cell receptor consisting of NKp30, useful in preparing a composition for treating a neoplastic disease.

Claim 5; SEQ ID NO 4; 66pp; English

The present invention describes a polypeptide conjugate comprising: (a) a target recognition segment comprising a natural killer cell receptor (NCR) or its fragment that binds to a cellular ligand expressed on the surface of a target tumour cell; and (b) a second segment comprising an active agent capable of exerting a cellular ligand expressed on the surface of a target tumour cell; and (b) a second segment comprising an active agent capable of exerting a corporative effect on the target cell. Also described: (l) an isolated polymucleotide encoding the polypeptide conjugate; (2) a vector and capable of expressing the polypeptide conjugate; (4) a pharmaceutical composition comprising the polypeptide conjugate and a carrier, stabiliser or diluent; (5) treating a neoplastic disease in a subject; (6) inhibiting the growth of a tumour cell in a subject; and (7) delivering a cytotoxic substance to a target tumour cell in a subject; and (7) delivering a cytotoxic substance to a target tumour cell in a subject. The polypeptide conjugate has cytostatic activity, and can be used in gene therapy. The polypeptide conjugate is useful in preparing a composition for treating a copyreptide conjugate is useful in preparing a composition for treating a copyreptide conjugate sease associated with a solid tumour or a non-solid tumour, e.g., carcinomas, melanomas, gliomas, neuroblastomas, Bellomas, neuroblastomas, Bellomas, Collid tumour or laurel a human natural cell corporation. killer cytotoxicity receptor conjugate, designated NKp30-Fc conjugate, which is used in the exemplification of the present invention.

Example; SEQ ID NO 14; 86pp; English.

malignant tumors.

Sequence 382 AA;

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5
                                                                             54
                                                                             ---ALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVT
                                        9
57.0%; Score 608.5; DB 8; Length 382; 85.8%; Pred. No. 3.9e-49; ive 5; Mismatches 6; Indels 9;
                   85.8%;
                                                                           1 MAWMLLLILIMVHPGSC-
                     Best Local Similarity 85.8
Matches 121; Conservative
                   Local Similarity
 Query Match
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68 WPRDEVVPGKEVRNGTPEFRGRLAPLASSRPLHDHQAELHIRDVRGHDASIYVCRVEVLG 127 natural cytotoxicity receptor; natural killer cell; lymphocyte; membrane; tumor; cell disintegration; antibody; NKp30; hyperproliferation; cytostatic; IgG1; CD5; fusion protein. 11 LATLYLLGMLV---ASCLGRLRVPLWVSQPLEIRTLEGSSAFLPCSFNASQGRLAIGSVT 67 New peptides derived from specific natural cytotoxicity receptors and capable of binding to membrane-associated biomolecules of tumor cells. useful for targeting tumor cells to diagnose or treat benign and/or (YISS ) YISSUM RES & DEV CO. (UYNE ) UNIV BEN-GURION NEGEV RES & DEV. Human CD5-NKp30-IgG1 Fc fusion protein. LGVGTGNGTRLVVEKEHPQLG 135 128 LGVGTGNGTRLVVEKEHPQLG 148 AEA40208 standard; protein; 382 AA 24-NOV-2004; 2004WO-IL001081. 25-NOV-2003; 2003US-0524648P Mandelboim O, Porgador A; (first entry) 2005-405348/41. N-PSDB; AEA40218. WO2005051973-A2. Homo sapiens. 11-AUG-2005 09-JUN-2005 Synthetic. AEA40208; 55 115 셤 ò g ð

The invention relates to isolated peptide fragments of a natural cytotoxicity receptor (NCR) of natural killer (NK) cells, or active cytotoxicity receptor (NCR) of natural killer (NK) cells, or active cragable of binding to a membrane-associated biomolecule of a tumor cell, and the biomolecule comprises at least one sulfated polysaccharide, and serves as the binding site of the NCR mediating the lysis of tumor cells by NK cells, with the proviso that the peptide is other than a full length NCR polypeptide or an isolated NCR extracellular domain. Also described are: (1) an antibody that recognizes an epitope on a target membrane-associated biomolecule of a tumor cell; the biomolecule comprising at least one sulfated polysaccharide and mediating the lysis of tumor cells by NK cells via the NCR; (2) a method of targeting a tumor cell by NK cells via the NCR; (2) a method of targeting a tumor cell by NK cells via the NCR; (2) a method of binding to a membrane-associated sulfated polysaccharide of a tumor cell. The peptide cell in a subject via an NCR velocation of NCR which are capable of binding to a membrane-associated sulfated polysaccharide of a tumor cell. The peptide cell in the specification (SEQ ID NOS: 1 and 2), or a fragment of the D2 domain of NKp46 comprising a sequence fully defined in the specification (SEQ ID NOS: 3 and 4). Alternatively, the peptide is a fragment of NKp46 is a fragment of NKp46 in the specification (SEQ ID NOS: 3). The having a sequence fully defined in the specification (SEQ ID NOS: 5). The

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membrane-associated biomolecule is selected from a glycosaminoglycan and a proteoglycan. The antibody is capable of blocking the binding of NK cells via NCR to membrane-associated sulfated polysaccharide biomolecules in a cell, therefore, inhibiting NCR-dependent cell lysis associated with autoimmunity. The peptides and antibodies of the invention are useful for targeting a tumor cell in a subject via an NCR-dependent mechanism. The composition and methods of the invention are useful for targeting tumor cells to diagnose and/or treat benign and malignant tumors or proliferative diagnose. This sequence represents a fusion protein computation human CDS leader sequence and human NKD30 D domain fused to the FC domain of human IgG1.
         8888888888888%&
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Sequence 382 AA;

68 WFRDEVVPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLG 127 WFRDEVVPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLG 114 1 MAWMLLILIMVHPGSC-----ALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVT 54 9; Gaps 57.0%; Score 608.5; DB 9; Length 382; 85.8%; Pred. No. 3.9e-49; tive 5; Mismatches 6; Indels 9 LGVGTGNGTRLVVEKEHPQLG 135 Query Match
Best Local Similarity 85.8
Matches 121, Conservative g 셤 ò ठे 8 8

Search completed: February 27, 2006, 17:59:07 Job time : 189 secs

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us-10-696-259-6.rpr

version 5.1.7 - 2006 Biocceleration Ltd. GenCore (c) 1993 Copyright

- protein search, using sw model OM protein

February 27, 2006, 17:59:23; Search time 40 Seconds (without alignments) 483.489 Million cell updates/sec Run on:

US-10-696-259-6 1067 1 MAWMLLLILIMVHPGSCALW......APLPPPCGSSAHLLPPVPGG 201 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR 80:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ρ	T-cell receptor al	T-cell receptor al	Iq lambda chain -	cytotoxic T-lympho	T-cell receptor be	membrane-bound imm	cytotoxic T-lympho	Ig lambda chain -	CTLA-4 precursor -	Ig lambda chain -	T-cell receptor al	_		T-cell receptor al	T-cell receptor al	д	T-cell receptor al	Ig lambda chain -	T-cell receptor al		T-cell receptor al	cytotoxic T-lympho	Ig lambda chain -	sialoadhesin - mou	T-cell receptor al	T-cell receptor al		А	cell receptor
ID	B45893	A24402	S25756	T09536	S26408	A46477	A29063	S25747	146696	S25749	C27577	D24092	E24092	RWMSAV	F45893	S09713	A42692	S14675	B24092	S36325	I54487	S08614	S25746	S50065	A24092	A53268	A31211	S24319	S21826 ·
DB	5	~	~	~	N	~	~	~	~	~	~	7	~	-	7	~	~	N	~	~	~	~	7	~	~	N	~	N	0
gt	136	3	m	N	4	N	223	m	N	m	m	131	m	132	131	m	2	235	110	139	120	186	236	1694	110	271	130	128	152
Query Match	11.1	11.0	11.0	10.9	10.9	10.9	10.8	10.6	10.3	10.3	10.1	10.0	10.0	6.6	9.8	9.8	9.7	9.7	9.6	9.5	٠	9.5	9.4	9.4	9.4	9.3	9.3	9.5	9.5
Score	1	117.5	117.5	116.5	116	116	115	113	110	110	107.5	106.5	106.5	106	105	104.5	103	103	102.5	101.5	101	101	100.5	100.5	100	99.5	66	98.5	98.5
Result No.	-	7	m	4	ហ	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

myelin/oligodendro	butyrophilin precu	Ig lambda chain pr	T-cell receptor al	Ig lambda chain pr	myelin/oligodendro	T-cell receptor al	myelin/oligodendro	Ig lambda chain pr	T-cell receptor al	T-cell receptor al	Ig lambda chain -	myelin P0 protein	T-cell receptor al	ARMVlambda protein	T-cell receptor de
A55717	S70587	LEHUEB	D24402	PH0134	B47712	JH0342	S58394	805270	168824	D45893	S25759	A32999	RWMSC8	842610	836302
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247	526	131	131	140	218	108	247	235	117	132	235	246	267	136	139
9.5	9.5	9.0	9.0	0.6	0.6	8.9	8.9	8.8	8.7	8.7	8.7	8.7	8.7	8.7	8.7
98.5	98.5	96	96	95.5	95.5	94.5	94.5	94	93	93	93	93	93	92.5	92.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

Tacell receptor alpha chain precursor V region (BTA29) - bovine
C;Species: Bos primigentus taurus (cattle)
C;Species: Bos primigentus taurus (cattle)
C;Accession: B45893 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000
C;Accession: B45893
R;Ishiquro, N.; Tanaka, A.; Shinagawa, M.
Imunogenetics 31, 57-60, 1990
A;Reference number: A5893; MUD:90129157; PMID:2137108
A;Reference number: A5893
A;Accession: B45893
A;Accession: B45893
A;Status: preliminary
A;Residues: 1-136 <1SH>A;Accession: B45893
A;Cross-references: UNIPARC:UPI000011D089; GB:D90011; NID:g217610; PIDN:BAA14061.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

ģ 42; Length 136; ch 11.1%; Score 118; DB 2; Length 136 Similarity 27.9%; Pred. No. 0.0036; 41; Conservative 22; Mismatches 42; Indels Query Match Best Local Si Matches 41,

57 RDEVVPGKEVRNGTPEF------RGRLAPLASSRFLHDHQAELHIRDVRGHDASI 105 99 57 4 MLLLILIMV------HPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWF d ò ઠે

58 RQ--YPGK-----GPEFLLQVYANNNKEEGKFT--AQSNKTNKH-VSLRIRDSEPSDSAT 107 셤 ð

106 YVCRVEVLGLGVGT----GNGTRLVVE 128 g

T-cell receptor alpha chain precursor V region (C5) - mouse (fragment)
T-cell receptor alpha chain precursor V region (C5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 30-May-1997
C;Accession: A24402
R;Becker, D.M.; Patten, P.; Chien, Y.; Yokota, T.; Eshhar, Z.; Giedlin, M.; Gascoigne, Nature 317, 430-434, 1985
A;Title: Variability and repertoire size of T-cell receptor V-alpha gene segments.
A;Reference number: A93368; MUD:86014379; PMID:2995827
A;Accession: A24402
A;Accession: A24402
A;Accession: A24402
A;Accession: A24402
A;Accession: A24402
A;Cross-references: UNIPARC:UPI00001768DA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

7;

Gaps

29;

82

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C;Accession: $26408
R;Bowman, S.J; Lanchbury, J.S.
submitted to the EMBL Data Library, September 1992
A;Description: T cell receptor beta chain sequences from patients with rheumatoid arthri
A;Reference number: $26408
A;Accession: $26408
A;Access
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 EVVPG-----KEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 EVRNGTPEFRGRLAPLASSRFLHD------HQAELHIRDVRGHDASIYVCRVEVL-- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLLRA----GFYAVSFLSVAVGSTVYYQGKCLT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 PPYYLGIGNGTQIYVIDPEPCPDSDFLLWILAAVSSGLFFYSFLLTAVSLS-----KMLK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell receptor beta chain V region (5.5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAWMLLLILIMVHPGSCALWVSQPPE--IRTLEGSSAFLPCSFNASQGRLAIGSVTWFRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 LLFFLLFIPVFCKAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRQADSQVT
                     A;Gene: CTLA4
A;Map position: 2q33
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C;Keywords: T-cell; transmembrane protein
                                                                                                                                                                                                                                                                   Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 116; DB 2; Length 146; 26.5%; Pred. No. 0.0058; tive 26; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                              Query Match 10.9%; Score 116.5; DB 2; Best Local Similarity 27.0%; Pred. No. 0.0084; Matches 54; Conservative 24; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 EVLGLGVGT-----GNGTRLVVEKE 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 WKGPRRQLPAVVPAPLPPPC 188
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Best Local Similarity 26.5%
Matches 39; Conservative
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Granda chain - human immunoglobulin lam
Aritle: V(lambda) and J(lambda) - C(lambda) gene segments of the human immunoglobulin lam
Aritle: V(lambda) and J(lambda) - C(lambda) gene segments of the human immunoglobulin lam
Aritle: V(lambda) and J(lambda) - C(lambda)
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Aritle: V(lambda) and J(lambda) - C(lambda)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytotoxic T-lymphocyte protein 4 - human cytototoxic T-lymphocyte protein 4 - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09536
R;Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P. J. Immunol. 147, 1037-1044, 1991
A;Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both management T09536
A;Accession: T09536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Goldel type: mRNA
A;Reference mNNA
A;Reference T1-223 cmNA
A;Reference T1-230 cmNA
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57 K--PGQAPVLVVYDDSDRPSGIPERFSGSNS-----GNTATLTISRVEAGDEADYY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVVPGK------EVRNGTPE-FRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRVEVLGLGVGTGNGTRLVV--------EKEHPQLGAGTVLLLRAGFY--AVS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                                                                                                                                                                                                                         LHVSLVFLWLQLGGVSSQEKYQQSPESLIVPEGAMVSLNCSFSDS----ASQSIWWYQQH
                                                                                                                                                                                                                                                                                                                                                                                                                                          60 VVPGKEVR-----NGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEV
                                                                                                                                                                                                                                  -----VSQPPE-IRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDE
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                                DB 2; Length 132;
Score 117.5; DB 2; Pred. No. 0.0039; Indels
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Best Local Similarity 24.7%; Pred. No. 0.0072;
Matches 53; Conservative 27; Mismatches 74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VAWKADSSPVKAGVETTTP 184
                                     th 11.0%; Score 117.5; I Similarity 30.8%; Pred. No. 0.00344; Conservative 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 LGLGVGT---GNGTRLVVEKEHP 132
                                           Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                             12 VHPGSCALW-
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30; Gaps

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C;Species: Mus musculus (house)
C;Species: Mus musculus (house)
C;Species: Mus musculus (house)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C;Datesion: Application of the immunoglobulin superfamily--CTLA-4.
Nature 328, 267-270, 1987
Nature 328, 267-270, 1887
Nature 328, 267
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A,Residues: 1-36 <RES>
A,Crestreserreferences: UNIPARC:UPI000016CCDE; GB:M74362; NID:g192833; PIDN:AAA37489.1; PID
C,Genetics:
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                                                                                                                                                                                                                                                                                              GKEVRNGT--PEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
                                                                                                                                                                                                                                                                                                                                                                                G----NYTWPPEFLGP------GEDPNGTLIIQNVNKSHGGIYVCRVQEGNESYQQS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 MTEVCATTFTEKNTVGFLD--YPPCSGTF-NESRVNLTIQGLRAVDTGLYLCKVELMYPP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 PYFVGMGNGTQIYVIDPEPCPDSDFLLMILVAVSLGLFFYSFLVSAVSLS-----KMLKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NGTRLVVEKEHPQ----LGAGTV-LLLRAGFYAVSFLSVAVGSTVYYQGKCLTWKGPRRQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 --EVVPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVL--- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 GLGVGTGNGTRLVVEKEHPQLGAGTVL----LLRAGFYAVSFLSVAVGSTVYYQGKCLTW 169
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                                                    Gaps
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C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C;Keywords: transmembrane protein
                                               30;
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    27.3%; Pred. No. 0.0094;
ive 27; Mismatches 76; Indels
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RSPLTTGVYVKMPPTEPEC 211
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52; Conservative
                                           50; Conservative
Best Local Similarity
Matches 50; Conserv
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S25747
Ig lambda chain - human
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A; Residues: 1-68, 11, 70-226 <FLA>
A; Residues: 1-68, 11, 70-226 <FLA>
A; Cross-references: UNIPARC:UPI000016AB03; GB:M74721; NID:g337419; PIDN:AAA60270.1; PID:
R; Hashimoto, S.; Chiorazzi, N.; Gregersen, P.K.
Mol. Immunol. 32, 651-659, 1995
A; Title: Alternative splicing of CD79a (Ig-alpha/mb-1) and CD79b (Ig-beta/B29) RNA trans
A; Reference number: 157851; MUID:95371688; PMID:7643857
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-88, E',128-226 <HAS3>
A,Cross-references: UNIPARC:UPI000002A519; GB:S79248; NID:g1087006; PIDN:AAC60653.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-226 <LED>
A; Cross-references: UNIPARC:UPI000011398E; GB:S46706; NID:g257140; PIDN:AAB23558.1; PID:
A; Experimental source: Ly66 cell line
A; Note: gequence extracted from NCBI backbone (NCBIN:115213, NCBIP:115214)
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A; Residues: 1-226 <HA1>
A; Residues: 1-226 <HA1>
A; Residues: 1-226 <HA1>
A; Rotoss-references: UNIPARC; UPI000011398E; GB: U05259; NID: g452561; PIDN: AAA20495.1; PID:
A; Note: sequence extracted from NCBI backbone (NCBIN: 85180, NCBIP: 85181)
B; Flaswinkel, H.; Reth, M.
Immunogenetics 36, 266-269, 1992
A; Title: Molecular cloning of the Ig-alpha subunit of the human B-cell antigen receptor
A; Reference number: IS4496; MUID: 92347937; PMID: 1639443
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A;Residues: 1-88,'E',128-226 <KOY>
A;Cross-references: UNIPARC:UPI000002A519; EMBL:X83540; NID:g620080; PIDN:CAA58523.1; PI
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A.Introns: 27/1; 127/1; 166/3; 199/1
C.Complex: disulfide-linked heterodimer with Ig-beta; heterodimer associates non-covalent C.Complex: disulfide-linked heterodimer with Ig-beta; heterodimer associates non-covalent C.Keywords: alternative splicing; disulfide bond; glycoprotein; immunoglobulin; surface F;1-32/Domain: signal sequence #status predicted <SIG>F;3-24/Product: membrane-bound immunoglobulin Ig-alpha chain #status predicted <MAT>F;34-26/Product: membrane #status predicted <EMM>F;44-165/Domain: cxtracellular #status predicted <CYM>F;146-226/Domain: intracellular #status predicted <CYT>F;67,63,73,88;97,112/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI000011398E; GB:S75217; NID:9241773; PIDN:AAB20812.1; PID: A;Cross-references: UNIPARC:UPI000011398E; GB:S75217, NCBIE:75218)
R;Leduc, I.; Preud'homme, J.L.; Cogne, M.
Clin. Exp. Immunol. 90, 141-146, 1992
Clin. Exp. Immunol. 90, 141-146, 1992
A;Title: Structure and expression of the mb-1 transcript in human lymphoid cells. A;Reference number: A49135; MUID:93009083; PMID:1395095
                                                                 A; Molecule type: DNA
A; Residues: 1-226 <HAS1>
A; Residues: 1-226 <HAS1>
A; Residues: 1-226 <HAS1>
A; Cross-references: UNIPROT: P11912; UNIPARC: UPI000011398E; GB:L32754; NID: g600875; PIDN: R; Yu, L.M.; Chang, T.W.
R; Yu, L.M.; Chang, T.W.
J. Immunol: 148, 633-637, 1992
                                                                                                                                                                                                                                                                                     A,Title: Human mb-1 gene: complete cDNA sequence and its expression in B cells bearing A,Reference number: A46477; MUID:92105765; PMID:1729378
A,Accession: A46477
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J. Immunol. 148, 1556-1531, 1992
A;Title: Molecular cloning and expression pattern of a human gene homologous to the A;Reference number: A46479; MUID:92166394; PMID:1538135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.9%; Score 116; DB 2; Length 226;
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submitted to the EMBL Data Library, December 1994
A;Reference number: S51112
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A,Cross-references: GDB:133778; OMIM:600352
ccession: I54539
tatus: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
Residues: 1-226 <YU1>
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4

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C;Accession: $25749
R;Combriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamk, A;Reference number: $16439; WUID:91257162; PMID:1904362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: C27577; "C27557 Pircher, H.; Malker, C.L.; Michalopoulos, E.E.; Rupp, F.; H: R;Ivamoto, A.; Ohashi, P.S.; Pircher, H.; Walker, C.L.; Michalopoulos, E.E.; Rupp, F.; H: J. Exp. Med. 165, 591-600, 1997 A;Title: T cell receptor variable gene usage in a specific cytotoxic T cell response. Pr A;Reference number: A27557; MUID:87139812; PMID:3493320
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-235 <COM>
A; Residues: 1-235 <COM>
A; Cross-references: UNIPARC: UP10000115EPD; EMBL: X57814; NID: g33727; PIDN: CAA40951.1; PID
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 150-218/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 YC---VLYMGRGIVIFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 Q--TPGQAPRILMYNTNTRSSGVPDRFSGSIL-----GNKSALTITGAQAEDESDY 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 FRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVL-GLGVGTGNGTRLVVEKE 130
                                                                                                                                 Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell receptor alpha chain V region (5/10-20D) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVVPGKEVR------NGTPE-FRGRLAPLASSRFLHDHQAELHIRDVRGHDASIY
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A;Accession: C27557
A;Molecule type: mRNA
A;Residues: 22-138 <1W2>
A;Cross-references: UNIPARC:UP100001768DB; EMBL:X05733
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VAWKADSSPVKAGVETTTP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.3%; Score 110; DB 2; L. Best Local Similarity 23.7%; Pred. No. 0.032; Matches 52; Conservative 29; Mismatches 72;
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A; Residues: 1-138 < IWA>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 825747
Bur. J. Immunol. 21, 1513-1522, 1991
A;Itle: V(Iambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lam A;Ritle: V(Iambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lam A;Reference number: 816439; MUID:91257162; PMID:1904362
A;Accession: 825747
A;Status: preliminary; translation not shown
A;Roteuse type: mRNA
A;Residues: 1-33 *COM>
A;Cross-references: UNIPARC:UPI0000115EFB; EMBL:X57812; NID:933723; PIDN:CAA40949.1; PIL C;Superfamily: immunoglobulin V region; immunoglobulin homology <C;Roywords: heterotetramer; immunoglobulin homology <IMM>
F;148-216/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
146696
CTLA-4 precursor - rabbit
C; Species: Oryccolagus cuniculus (domestic rabbit)
C; Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C; Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C; Accession: 146696
R; Isono, T: Secto, A.
Imminogenetics 42, 217-220, 1995
A; Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecul
A; Reference number: 14689; MUID:95369849; PMID:7642234
A; Accession: 146696
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mesidues: 1-223 <180>
A; Cross-references: UNIPROT:P42072; UNIPARC:UPI000012862A; GB:D49844; NID:9755100; PIDN: C; Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RV-EVLGLGVGTGNGTRLVV-------EKEHPQLGAGTVLLLRAGFY--AVS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 VCAMTYTVENELTFIDDSTCTGISHGNKVNLTIQGESAMDTGLYICKVELMYPPPYYVGM 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 QKPGQAPVLVVYGDSDRPSGIPERFSGSNS-----GNTATLNISRVEAGDEAAYYC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRNGTPEFRGRLAPLASSR---FLHDHQAELHIRDVRGHDASIYVCRVEVL---GLGVGT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAWMLLLILIMVH-PGSCALWV-SQPPEIRTLEGSSAFLPCSFNASQG-RLAIGSVTWFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 10.6%; Score 113; DB 2; Length 233; Local Similarity 26.0%; Pred. No. 0.018; Local S6; Conservative 27; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 223;
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10.3%; Score 110; DB 2; Length 22:
Best Local Similarity 26.9%; Pred. No. 0.031;
Matches 52; Conservative 24; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VAWKADSSPVKAGVETTTP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 FLSVAVGSTVYYQGKCLTWKGPRRQLPAVVPAPLP 185
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Best Local S:
Matches 56
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-131 <15H>
A;Cose-references: UNIPARC:UPI000011D08D; GB:D90015; NID:g217618; PIDN:BAA14065.1; PID
A;Cross-references: UNIPARC:UPI000011D08D; GB:D90015; NID:g217618; PIDN:BAA14065.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;36-109/Domain: immunoglobulin homology <IWM>
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                                                                                                                                                                               76 RLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 135
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T-cell receptor alpha chain precursor V region (BTA25) - bovine (Species: Bos primigenius taurus (cattle) (C.5pecies: Bos primigenius taurus (cattle) (C.5pecies: 30-Sep-1993 #text_change 20-Jun-2000 (C.5pecession: F45893 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000 (C.5Accession: F45893) (S.5 Bhiguro, N.; Tanaka, A.; Shinagawa, M. Immunogenetics 31, 57-60, 1990 (Immunogenetics 31, 57-60, 1990 (A.; Tell receptor alpha chain. A); Reference number: A45893; MUID:90129157; PMID:2137108
         21 VSQPPEIRTL-EGSSAFLPCSFNASQGRLAIGSVTWF----RDEVVPGKEVRNGTPEFRG
                                                           24 VEQSPSALSLHEGTGSALRCNFTTT----MRAVQWFRKNSRGSLINLFYLASGTKE-NG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 9.9%; Score 106; DB 1;
Similarity 25.8%; Pred. No. 0.038;
10; Conservative 22; Mismatches 45,
                                                                                                                                                                                                                                                                                                                                                         136 AGTVL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                            122 QGTIL 126
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Best Local S:
Matches 40
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                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 01-Dec-2000 #text_change 11-Jan-2002
C;Accession: D24092; S03507
R;Fink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
R;Fink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
A;Title: Correlations between T-cell specificity and the structure of the antigen recept A;Reference number: A93380; MUD:86230843; PMID:3012351
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A; Residues: 1-131 < FINS
A; Residues: 1-131 < FINS
A; Residues: 1-131 < FINS
A; References: UNIPARC: UP10000176EBD
B; Winoto, A; Moleness, S; Hood, L.
Nature 316, 832-836, 1985
A; Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.
A; Reference number: $03503; MUID: 85296332; PMID: 2993908
A; Accession: $03507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Molecule type: DNA
A;Residues: 111-130 <MIN>
A;Crose-references: UNIPARC:UPI0000115274; EMBL:X03057; NID:g54519; PIDN:CAA26864.1;
A;Note: this sequence was determined from the germline gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: T-cell receptor
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-131/Product: T-cell receptor alpha chain V region B10 #status predicted <MAT>
F;36-109/Domain: immunoglobulin homology <IMM>
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-EGRFTIHLNKASLH---FSLHIRDSQPSDSALYLCAVSMTGGYKVVFGSGTRLLVSPD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Mus musculus (house mouse)
.Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 VEQSPSALSLHEGTGSALRCNFTTT-----MRAVQWFRKNSRGSLINLFYLASGTKE-NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 VSQPPEIRTL-EGSSAFLPCSFNASQGRLAIGSVTWF----RDEVVPGKEVRNGTPEFRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 131;
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-131 cFIN>
A.Cross-references: UNIPARC:UPI0000176E34
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: leceptor
C.Keywords: T-cell receptor
C.Keywords: Brain Bequence #status predicted cSIG>
C.Momain: signal sequence #status predicted cSIG>
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                                                                                                                                                                                                                    receptor alpha chain precursor V region (B10) - mouse
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Best Local Similarity 29.61
Matches 37; Conservative
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Query Match 9.8%; Score 105; DB 2; Length 131; Best Local Similarity 30.3%; Pred. No. 0.046; Matches 36; Conservative 23; Mismatches 34; Indels 26; Gaps
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Search completed: February 27, 2006, 18:03:48 Job time : 42 secs

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GenCore version 5.1.7

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2006, 17:56:08; Search time 230 Seconds

(without alignments)
616.570 Million cell updates/sec
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Title: US-10-696-259-6
Perfect score: 1067
Sequence: 1 MAWMLLLILIMVHPGSCALW......APLPPPCGSSAHLLPFVPGG 201
Scoring table: BLOSUM62

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 2166443 segs, 705528306 residues 2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt\_05.80:\* 1: uniprot\_sprot:\* 2: uniprot\_trembl:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	O14931 homo sapien	P61484 pan troglod	Q8mj02 macaca mula	P61483 macaca fasc	rattus	Q4zje7 canis famil	Q99mll mus musculu	Q28090 bos taurus	097631 ovis aries	Q6ipul homo sapien	homo	Q7tmx1 mus musculu	Q7jhj0 macaca neme	Q7jhj2 cercocebus		Q9bdn7 papio anubi			Q6gr94 homo sapien		Q6gtr6 mus musculu	Pli912 homo sapien	_	Q9gkp2 canis famil	_	Q9xsy7 felis silve	O9xtal felis silve	Q7tsu7 mus musculu	Q9jlv3 marmota mon		P42072 oryctolagus
	NCTR3 HUMAN	PANTR	MACMU	NCTR3 MACFA	RAT	7 CANFA	299M11 MOUSE	Q28090_BOVIN	1 SHEEP	1 HUMAN	3 HUMAN	Q7TMX1 MOUSE	0 MACNE	Q7JHJ2_CERTO	4_MACMU	7 PAPAN	HUMAN	5 HUMAN	Q6GR94 HUMAN	9 RAT	6_MOUSE	CD79A HUMAN	MOUSE	2 CANFA	QGGMV8_HUMAN	7 FELCA	29XTA1 FELCA	KIRR2 MOUSE	29JLV3_MARMO	PIG	CTLA4_RABIT
e e	NCTR3	NCTR3	NCTR3	NCTR3	NCTR3	042JE	Q99M1	02809	09763	QEIPU	OGGMW	O7TMX	Q7JHJ	Q7JHJ	Q9BDC	O9BDN	CTLA4	QS3TD	Q6GR9	06285	QGGTR	CD79A	CTLA4	Q9GKP	<b>O</b> 6GMV	Q9XSY	Q9XTA	KIRR2	09JLV	CTLA4	CTLA4
DB	1	-	-	н	-	~	7	~	~	~	7	~	~	7	N	~	-	~	~	~	~	-	-	~	~	N	~	-	~	-	7
Length	201	201	201	176	192	122	235	221	221	313	234	223	223	223	223	223	223	223	223	223	223	226	223	223	234	223	223	700	223	223	223
% Query Match	100.0	98.5	95.4	77.4	55.3	47.2	12.8	11.8	11.6	11.6	11.5	11.3	11.2	11.2	11.2	11.2	11.1	11.1	11.1	11.1	11.0	10.9	10.8	10.8	10.5	10.5	10.5	10.5	10.4	10.3	10.3
Score	1067	1051	1018	826	290	504	136.5	126	124	123.5	122.5	121		119	119	119	118.5	118.5	118.5	118	117	116	115	115	112.5	112	112	112	111	110	110
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Q9n186 sus scrofa Q96i69 homo sapien Q6dhw4 homo sapien Q6dgw4 homo sapien Q6dgw4 homo sapien Q9bdpl actus trivi Q6gmx4 homo sapien Q9hxa5 drosophila Q9hxa5 drosophila Q51xa6 homo sapien Q65ixa6 homo sapien Q65ixa6 mus musculu
Q9N186 PIG Q96169 HUMAN GGMU96 RAT QGMQ96 RAT QGMQ96 RAT QGMX3 HUMAN Q9BDP1 AOTTR GGMX4 HUMAN Q9YEVT DROME Q9WRA5 DROME Q9WRA5 DROME G59BZ1 DROME S1G13 FANTR S1G13 FANTR G53FBB HUMAN Q6PIQ7 HUMAN
попионичина
2223 2233 2233 2233 2224 2226 2326 1326 1326
000000000000000000000000000000000000000
110 110 110 109.5 108.5 108.5 108.5 108.5 108.5 108.5
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## ALIGNMENTS

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NUCLECTIDE SEQUENCE (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH TISSUE=Lymphoid;
TISSUE=Lymphoid;
MEDLINE=2002980;
Parolini S., Pessino A., Sivori S., Augugliaro R., Morelli L., Marcenaro E., Accame L., Malaspina A., Biassoni R., Bottino C., Moretta L., Moretta A.;
"Identification and molecular characterization of NKp30, a novel triggering receptor involved in natural cytotoxicity mediated by human natural killer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLECTIDE SEQUENCE (ISOFORMS 1; 2; 3; 4; 5 AND 6).
MEDLINE=99218514; PubMed=10202016;
Neville M.J., Campbell R.D.;
A new member of the Ig superfamily and a V-ATPase G subunit are among the predicted products of novel genes close to the TNF locus in the human MHC.";
J. Immunol. 162:4745-4754 (1999).
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                NCTR3 HUMAN STANDARD; PRT; 201 AA.
014931; 014930; 014932; 095667; 095668; 095669; Q5ST89; Q5ST90;
Q5ST91; 0SST92; Q5STA3;
05-JUL-2004 (Rel. 44, Loreated)
05-JUL-2004 (Rel. 44, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Natural cyrotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).
Name=NCR3; Synonyms=IC7;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identificastion of two novel single nucleotide polymorphisms in the NKp30 gene in human natural killer cells."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96422187; PubMed=8824804; DOI=10.1006/geno.1996.0034; Malabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.; "Genes in a 220-kb region spanning the TNF cluster in human MHC."; Genomics 31:215-222(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        χ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WITH CD3Z.
TISSUE=Peripheral blood;
Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Exp. Med. 190:1505-1516(1999).
                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
  HUMAN
NCTR3
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MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnss.242603899; MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnss.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altebrac R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altebrac R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altebrako L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F., Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C., Arpheton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., Arpheton M.J., Wckernan K.J., Malek J.A., Gunaratne P.H., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Allalon D.K., Muzuy D.W., Soderjeen B.J., Lu X., Gibbs R.A., Willalon D.K., Muzuy D.W., Soderjeen B.J., Lu X., Gibbs R.A., Willalon D.K., Muzuy D.W., Soderjeen B.D., Lu X., Gibbs R.A., Wilting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Mhiting M., Madan A., Young A.C., Schwutz J., Myers R.M. C., Abriech B. C., Grimwood J., Schmutz J., Myers R.M., C., Shailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E., Jones S.J.M., Marra M.A., Scheit J. Hength human D.M., Gaben E.D., Dickson M.C., Smailus D.E., Gordenteation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                      Widteotide Sequence [Large SCALE GENOMIC DNA],

RAPA MEDISTR=22937573; Dubded=1457464; DOL=10.1038/nature02055;

RADINE=2297573; Dubded=1457464; DOL=10.1038/nature02055;

RADINE=2297573; Dubded=1457464; DOL=10.1038/nature02055;

RADINE SEATOR M.C., Horton R., Hunt S.E., Scott C.E.,

RADINE J. Jones M.C., Horton R., Hunt S.E., Scott C.E.,

RADINE J. Jones M.C., Horton R., Hunt S.E., Scott C.E.,

RADINE J. Seates K., Beare D.M., Beasley M., Braker D.J.,

RADINE SE., Bray-Allen S., Brook J., Brown J.C., Earler W.P.,

RADINE SE., Burrill M., Burcon J., Carter W.D.,

RADINE R.E., Collins J.E., Colman L.K., Corby N.R., Covile G.J.,

RADINE R.E., Evench L., Garrer P., Grafham D.V., Frankish A.,

Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,

Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,

Ellington A.E., Evans K.A., Gatthero R.J., Grafham D.V., Grafham D.V., Grait M.J.,

RADINE S., Griffiths C., Glitthero R.J., Grafham D.V., Grant M.J.,

RADINE S., Griffiths C., Glitthero R.J., Grafham D.V., Grant M.J.,

RADINE S.J., Howden P.J., Howe K.L., Howell G.R., Hach C.E.,

RADING S.J., Howden P.J., Howe K.L., Howell G.R., Lloyd D.M.,

RADING S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,

LAWLOR S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,

RADING S., Loongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,

RADING S., Loongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,

RADING S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,

ROVELEM G.L., Matthews L., McCann O.T., Mashreghi-Mohammadi M.,

ROVIK K.L., Thomas D.W., Thorpe A., Tromans A., Tromans A., Thoby S.,

RADINE S., Reward C.A., Stewer C.D., Smith M., Spragon L.,

ROVIK K.L., Thomas D.W., Thorpe C.S., Thomas D.W., Thorpe C.S., Milmet S., Matthew M., Walle S., Matthew M., Mille S., S., Milmet S., Sulth M., Watther S., Thomas D.W., Thorpe A., Tromans D.W., Thorpe A., Tromans J., Buntley D.J., Wallmer T.R., Noole S.,

RADINE M., Watther S., Sulth M., Watther M., While S.,

RADINE 
PubMed=14656967; DOI=10.1101/gr.1736803; Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S., Campbell R.D., Hood L.; Hood L.; Hood L.; Fhe gene-dense major histocompatibility complex class III region and its comparison to mouse."; Genome Res. 13:2621-2636(2003).
                                                                                                                                                                                                          NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
Shijna S., Tamiya G., Oka A., Inoko H.;
"HGmo sapiens 2,229, 817bp genomic DNA of 6p21.3 HLA class I region.";
submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Durbin R., Hubbard T., Sulaton J.E., Dunham I., Fogers "The DNA sequence and analysis of human chromosome 6."; Nature 425:805-811(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
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THE SERVER SERVE

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis energy subbunit: Interacts with CD3Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOId=014931-6; Sequence=VSP_010411, VSP_010412;
NOTe=NO experimental confirmation available;
-!- TISSUE SPECIFICITY: Selectivelly expressed by all resting and activated NK cells and weakly expressed in spleen.
-!- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR)
                                                                    -:- SUBGNIT: Interacts with CD3Z.
-:- SUBGNIT: Interacts with CD3Z.
-:- ALTERNATIVE PRODUCTS:
-:- Name=1; Synonyms=1C7a;
-:- Isold=014931-1; Sequence=USP 010413;
-:- Isold=014931-2; Sequence=USP 010412;
-:- Nome=3; Synonyms=1C7b;
-:- Nome=4; Synonyms=1C7b;
-:- Isold=014931-3; Sequence=USP 010411;
--- Nome=4; Synonyms=1C7f;
--- Isold=014931-4; Sequence=USP 010411;
--- Nome=5; Synonyms=1C7f;
--- Isold=014931-5; Sequence=USP 010411, VSP 010413;
--- Nome=5; Synonyms=1C7f;
--- Isold=014931-5; Sequence=USP 010411, VSP 010412;
--- Name=5; Synonyms=1C7f;
--- Isold=014931-5; Sequence=USP 010411, VSP 010412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
-!- CAUTION: Ref.7 (CA117692, CA118306, CA118664 and CA141957)
sequences differs from that shown due to erroneous gene model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -; Genomic_DNA.
-; Genomic_DNA.
ALT_SEQ; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB86580.1; -; mRNA.
AAD18088.1; -; Genomic_DNA.
BAB63393.1; -; Genomic_DNA.
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Y14768; CAA75064.1; -; Genomic_DNA.
Y14768; CAA75066.1; -; Genomic_DNA.
Y14768; CAA75066.1; -; Genomic_DNA.
Y14768; CAA75067.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB86579.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ223153; CAB54004.1; -; mRNA.
EMBL; AB055881; BAB78472.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF031136; AAB86578.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL662801;
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EMBL;
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CAI41956.1; CAI41957.1;

BX248519;

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Name=5
               CARBOHYD
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  CARBOHYD
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Best Local
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                                                                                                                                                              61 VPGKEVRNGTPEFRGRLAPLASSRPLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
                                                                                                                                                                                                                   NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGKCLTWKGPRRQLPAVV 180
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                            1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEV
                                                                                                          VPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG LIKE; 1.
Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.
SIGNAL 1 18 Potential.
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Natural cytotoxicity triggering receptor
                                                                  Gaps
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10-MAY-2005 (Rel. 47, Last annotation update)
Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of natural killer receptors in chimpanzees.";
Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells mediate tumor cell lyais (By similarity).
-!- SUBUNIT: Interacts with CD32 (By similarity).
-!- SUBCELDULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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0
                                         Length 201;
                                                                  Indels

    Extracellular (Potential)

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Cytoplasmic (Potential)
Ig-like.
                                         DB 1;
                                       100.0%; Score 1067; DB 1;
100.0%; Pred. No. 1.6e-83;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         201 AA
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InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
EMBL; BC052582; AAH52582.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                         PAPLPPPCGSSAHLLPPVPGG 201
                                                                                                                                                                                                                                                                        05-JUL-2004 (Rel. 44, Created)
                                                    Best Local Similarity 100.
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                        STANDARD:
            HGNC; HGNC:19077; NCR3.
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156
201
126
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SMART; SM00409; IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lymphoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9598;
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136
157
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                                                                                                                                                                                                                                                                                                                                     NCTR3 PANTR
ID NCTR3 PANTR
AC P61484;
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                                                                                                                                           1 MAWMILLILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEV
                                                                                                                                                             1 MAMMLLILILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEV
                                                                                                                                                                                                          VPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCTR3 MACMU STANDARD; PRT; 201 AA.
OBMJ02; OSTM24; OBMJ00; OBMJ01; Q95JB8;
05-JUL-2004 (Rel. 44, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Natural Cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15269276; DOI=10.1093/molbev/msh216; Kulski, J.K., Anzai T., Shiina T., Inoko H.; Macaque class I duplicon structures, organization, and evolution within the alpha block of the major histocompatibility
N-linked (GlcNAc. ..) (Potential)
N-linked (GlcNAc. ..) (Potential)
                                                                                                              ö
                                                                              Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 4), AND VARIANT VAL-156
                                                                                                            2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rizzi M., Blassoni R.;
"NCR express by macaca NK cells.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                              / similarity.
3768ACC768E8D749 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         013642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=5;
                                                                             Score 1051; DB 1;
Pred. No. 3.7e-82;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q8MJ02-1; Sequence=VSP_013641, VSP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q8MJ02-5; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                      181 PAPLPPPCGSSAHLLPPVPGG 201
                                                                                                                                                                                                                                                                                                                                                        PAPLPPPCGSSAQLLPPVPGG 201
                               ВУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque).
42 N-
121 N-
108 By
21656 MW;
                                                                             98.5%;
                                                                                            al Similarity 99.0
199; Conservative
42
121
39
1
201 AA;
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181 PAPLPPPCGSSAHLLPPVPGG 201
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136
157
                                                                                                                                                                                                                                                                                          TISSUE=Lymphoid;
                                                                                         NCTR3 MACFA & P61483; Q95JB8;
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                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                          Natural cytotoxicity triggering receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTWKGPRROLPAVV -- HCHMGTHCHSSDGP (in
                                                                                  Isold=QBMJ02-4; Sequence=VSP_010417; Note=No experimental confirmation available; SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR)
                                                                                                                                   SIMILARITY: Contains 1 1g-like (immunoglobulin-like) domain.
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N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
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                                                                                                                                                                                                                                                                                                                                                                   SMART; SMOUGUS; 10. LIKE; 1. PROSITE; PS50835; IGLIKE; 1. Alternative splicing; Glycoprotein; Immunoglobulin domain; Alternative splicing; Glycoprotein; Transmembrane.
Polymorphism; Receptor; Signal; Transmembrane.

18 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 AA; 21684 MW; AE3A325C8585BA68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> NILS (in isoform
                                           IsoId=08MJ02-3; Sequence=VSP_010415; VSP_010416;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTIG=VSP 010415.
Missing (in isoform 3).
/FTIG=VSP 010416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wissing (In isoform 4). /FIId=VSP 010417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform 2).
     IsoId=Q8MJ02-2; Sequence=VSP_010414;
Note=No experimental confirmation available;
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                                                                                                                                                                                                                                         EMBL; AY035214; AAK63116.1; -; mRNA.
EMBL; AY035215; AAK63117.1; -; mRNA.
EMBL; AY035217; AAK63118.1; -; mRNA.
EMBL; AX035217; AAK63118.1; -; mRNA.
EMBL; AX554301; CAD86942.1; -; mRNA.
EMBL; AJ128049; BAD69721.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing
                                                                                                                                                                                                                                                                                                                        HSSP; p16410; 1185.
InterPro; IPR0013599; 19.
InterPro; IPR007110; 19-like.
SMART; SM00409; 1G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 95.0 Matches 191; Conservative
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124
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rizzi M., Biassoni R.;
"Non MHC specific natural cytotoxicity receptors (NCR) expressed in Macaca fascicularis lymphoid cells.";
Macaca fascicularis lymphoid cells.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).
-!- SUBWIT: Interacts with CD3Z (By similarity).
-!- SUBWIT: Interacts with CD3Z (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAWMALALILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
SWART; SM0409; IG; I.
PROSITE; PS50835; IG LIKE; I.
Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
Natural cytotoxicity triggering receptor
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                                                                                                                                                                                                      05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Natural cytocoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).
Name=NCR3;
                                                                                                                                                                                                                                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Butheria; Buarchontoglires, Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.4%; Score 826; DB 1; Length 176; 95.2%; Pred. No. 6.7e-63; ive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extracellular (Potential).
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97B2A3B625E4AD54 CRC64;
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Cytoplasmic (Potential).
                                                                                                                                                         176 AA.
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HSSP; P16410; 1185.
                                                                                                                                                         PRT;
181 PGPLPPPCGSSAHLLPPVPGG 201
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Matches 158; Conservative
                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
176
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42
121 1
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Gaps

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61 VPGKEVRNGTPEFRGRLAPLASSRPLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LWVFQPPEIHTQEGTAAFLPCSFNASERKLAIGSVTWYRDKVAPGKEVRNGTPEFRGRLA 60
                                                                                                                                                                                                                                                                                                                                    1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 LWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLA
               Potential.
Natural cytotoxicity triggering receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGTRLVVEKEHPQ-----LGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGKCLTWKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                     Ig-like.
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
                                                                                                                                                                                                                                                                        DB 1; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 122;
                                                                                                                                                                                                                                                                      55.3%; Score 590; DB 1; Length 19
64.2%; Pred. No. 1.3e-42;
ive 24; Mismatches '32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chu R., Lin Y.-C., Wang Y.-S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; DQ003484; AAY21817.1; -; mRNA.
                                                         Extracellular (Potential).
                                                                                                                                                                                          A -> V.
A -> T.
A -> V (in Ref. 2).
7 7FC84F8252D22377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 122
122 AA; 13307 MW; FB14BD6B314279DA CRC64;
                                                                        Potential.
Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                   By similarity.
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                      Best_Local Similarity 64.2
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q4ZJE7_CANFA PRELIMINARY;
Q4ZJE7;
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168
192
126
121
108
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82
138
135
195 AA;
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VL 122
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Transmembrane
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CARBOHYD
DISULFID
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CONFLICT
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=2216#131; PubMed=12180816; DOI=10.1016/S0966-3274(02)00033-3; H8ieh C.L., Obara H., Ogura Y., Martinez O.M., Krams S.M.; "NK cells and transplantation."; "Transpl. Immunol. 9:111-114(2002).
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                              QBCFD5; QBOWMB; QBCG11; 05-Jul-2004 (Rel. 44, Created) 05-Jul-2004 (Rel. 44, Last sequence update) 13-SEP-2005 (Rel. 48, Last sequence update) Natural cyrotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR003599; Ig.
Interpro; IPR007110; Ig-1ike.
SMART; SM00409; IG; 1.
PROSTIR; PS50835; IG LIKE; 1.
Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells mediate tumor cell lypis (By similarity).
-!- SUBUNIT: Interacts with CD3Z (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Brown Norway;
PubMed=15060004; DOI=10.1101/gr.1987704;
Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
"The genomic sequence and comparative analysis of the rat major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular characterization of the novel rat NK receptor 1C7.";
Eur. J. Immunol. 33:342-351(2003).
                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE, AND VARIANTS VAL-7; VAL-19; VAL-82 AND STRAIN-PVG; TISSUE-Natural killer cell; PubMed=12548565; DOI=10.1002/immu.200310008; Backman-Petersson E., Miller J.R., Hollyoake M., Aguado B., Butcher G.W.;
         NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGKC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ430418; CAD23066.1; -; MRNA.
EMBL; AJ430419; CAD23067.2; -; Genomic_DNA.
EMBL; AJ430420; CAD23067.2; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensembl; ENSRNOG0000000854; Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                     Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY273824; AAP13457.1; -; mRNA.
BX883046; CAE84000.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        histocompatibility complex.";
Genome Res. 14:631-639(2004).
                                                                                                                STANDARD;
                                                                                                                                                                                                                                        Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                              NCTR3 RAT
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112 SYSSGIRV-FGGGTKLTV 128

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Query Match
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                     RESULT
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                                                                                                                                                                                                                            TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

XX MEDLINE=2238825; PubMed=12477922; DOI=10.1073/pnas.242603899;

XX MEDLINE=22388257; PubMed=12477922; DOI=10.1073/pnas.242603899;

XX Altashul S.P., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,

XA Altashul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.P., Zeeberg B., Barana J., Marshin G.M., Hong L.,

A Batchanto, L., Marusin B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EVVPGKEVRNG--TPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAWMILLILIMVH-PGSCA-LWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Gaps
                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 235;
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Strausberg R.;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002129; AAH02129.1; -; mRNA.
HSPP; PO1843; JUNH.
GO; GO:0003823; F:antigen binding; IEA.
InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003596; Ig-cl.
InterPro; IPR003596; Ig-VHC.
Pfam; PF07654; C1-8et; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0835; IG_LIKE; 2.
PROSITE; PS00209; IG_MHC; UNKNOWN 1.
Hypothetical protein; MMLIOGIObulin domain.
BEQUENCE 235 AA; 25403 NW; 39807BFE6782A3FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 12.8%; Score 136.5; DB 2; Local Similarity 31.2%; Pred. No. 0.0014; hes 43; Conservative 25; Mismatches 49;
                          PRT;
                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 VEVLGLGVGTGNGTRLVV 127
                                                       01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                       Q99M11_MOUSE PRELIMINARY;
Q99M11;
                                                                                                 Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Czech II;
                                                                                                                                                                                                                          STRAIN-Czech II;
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               MOUSE
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Matches
RESULT 7
Q99M11_MO
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66 VRNGTPEFRGRLAPLASSRFL---HDHQAELHIRDVRGHDASIYVCRVEVL---GLGVGT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 GNGTQIYVIDPEPCPDSDFLLWILAAVSSGLFFYSFLITAVSLS-----KMLKKRSPLTT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 LPFLVPIPVFSKGMNVTQPPVVLASSRGVASFSCEYESS-GKADEVRVTVLKEAGSQVTE 81
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96186531, PubMed-8606060; DOI=10.1007/8002510050080; Parsons K.R., Young J.R., Collins R.A., Howard C.J.; "Cattle CTLA-4, CD28 and chicken CD28 bind CD86: MYPPPY is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 11.8%; Score 126; DB 2; Length 221; Local Similarity 27.5%; Pred. No. 0.011; hes 53; Conservative 26; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2CAF148422C597AA CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytotoxic T-lymphocyte-associated protein 4.
Name=CTLA-4;
                                                                                                                                                  Last sequence update)
Last annotation update)
221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved in cattle CD28.";
Immunogenetics 43:388-391(1996).
EMBL; X93305; CA63708.1; -; mRNA.
HSSP; P16410; 1185.
SMR; Q28090; 35-159.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
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                                                                                                        Created)
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pram; Frecon, Pramingen, PRINTS; PRO1720; CTLANTIGEN4. SMART; SM00409; IG; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin domani; Signal 185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 221 AA; 24433 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008096; CTLA4.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                   01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 LPAVVPAPLPPPC 188
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Q28090 BOVIN PRELIMINARY;
Q28090;
                                                                                                                                                                                                                                                                CTLA-4 protein precursor.
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097631 S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GNGTRLVVEKEHPQLGAGTVLLLRA----GFYAVSFLSVAVGSTVYYQGKCLTWKGPRRQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Abukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                              6 LLILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetecow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                      MUCLEOTIDE SEQUENCE.
MEDLINE=99309828; PubMed=10380709; DOI=10.1007/8002510050542;
Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;
"Cloning and sequence comparison of sheep CD28 and CTLA-4.";
"Immunogenetics 49:583-584[1999].
-I- FUNCTION: Not known (By similarity).
-I- SUBUNIT: Associates non-covalently with beta-2-microglobulin (By
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                      11.6%; Score 124; DB 2; Length 221; 26.9%; Pred. No. 0.016; ive 27; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                          221 AA; 24490 MW; D317E9D5557BA6FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-UUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 AA.
                                                                                                                                     BMBL; AF092740; AAD04380.1; -; mRNA. HSSP; HSP097410; 1185. SMR; O97631; 35-159. GO; GO: 0016020; C: membrane; IEA. GO; GO: 0006955; P: ; mmune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                PRINTS; PR01720; CTLANTIGEN4.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
                                                                                                                                                                                                                                            InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                         InterPro; IPR008096; CTLA4.
InterPro; IPR003599; Ig.
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                                                                                                                                                                                                                                                                                                                                                                                                  52; Conservative
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QEIPUL;
                                                                                                                                                                                                                                                                  Pfam; PF00047; 19; 1.
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
          NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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59 EVVPG-----KEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRV 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Shein Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                           1 MAWMLLLILIMVHPGSCALWVSQPPE--IRTLEGSSAFLPCSFNASQGRLAIGSVTWFRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 EVLGLGVGT----GNGTRLVV-------EKEHPOLGAGTVLLLRAGFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 11.6%; Score 123.5; DB 2; Length Similarity 25.7%; Pred. No. 0.026; 46; Conservative 26; Mismatches 62; Indels
                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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QGGMW3;
                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 E-----VVPGKEVR-NGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 -----EVLGLGVGTGNGTRLVV-------EKEHPQLGAGTVLLLRAGFY--A 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 WHGSSEVI---LVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAWMILLILIMVH-PGSCALWV-SOPPEIRTLEGSSAFLPCSFNASOGRIAIGSVTWFRD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.P., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heltron E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Onoes S.J.M., Marza M.A., Schein J.E., Garman A., Marza M.A., Schein J.E., Garman A., Schain J.E., Marza M.A., Schain J.E., Garman A., Schain J.E., Marza M.A., Schain J.E., Marza M.A., Schain J.E., Marza M.A., Schain J.E., Garman A., Garm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 234 AA; 24653 MW; 52339D4FF0E6BB97 CRC64;
                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytotoxic T-lymphocyte-associated protein 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 VSFLSVAVGSTVYYQGKCLTWKGPRRQLPAVVPAPLP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 11.5%; Score 122.5; DB 2; Local Similarity 26.3%; Pred. No. 0.023; es 57; Conservative 27; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC073787; AAH73787.1; -; mRNA.
SMR; Q6GMW3; 21-234.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; IG.
InterPro; IPR003110; IG-11ke.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003599; Ig_C1.
InterPro; IPR003596; Ig_W.
Pfam; PF07654; C1-set; T.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 2.
SWART; SW00406; IG; 1.
PR0SITE; PS50835; IG LIKE; 2.
WROSITE; PS00290; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Q7TMX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Primary B-Cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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Q7TMX1 MOU
ID 77 TMX
AC Q7TMX
AC Q7TMX
DT 01-0C
DT 01-0C
DT 01-MM
BE CYCOT
GN MUS FE
COT 
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81 MTBVCATTFTEKNIVGFLD--YPFCSGTF-NESRVNLTIQGLRAVDTGLYLCKVELMYPP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 --EVVPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVL--- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 GLGVGTGNGTRLVVEKEHPQLGAGTVL----LLRAGFYAVSFLSVAVGSTVYYQGKCLTW 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 WMLLLILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.3%; Score 121; DB 2; Length 22;
Best Local Similarity 26.6%; Pred. No. 0.029;
Matches 53; Conservative 27; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Straugherg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC052683; AAH52683.1; -; mRNA.
HSSP; P09793; IDQT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSS6835; IG LIKE; 1.
Immunoglobulin domain.
SEQUENCE 223 AA; 25035 MW; EE8E4C77E6A04549 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CD152 protein precursor.
Name=CTLA-4;
Macaca nemestrina (Pig-tailed macaque).
STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P09793; IDCT.

SMR; Q7TMX1; 38-154.

MGI; MGI:8855; Ctla4.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0016021; C:extracellular space; TAS.

InterPro; IPR008096; CTLA4.

InterPro; IPR003599; IG-11ke.

PRINTS; PR01720; CTLANTIGEN4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 KGPRRQLPAVVPAPLPPPC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSPLTTGVYVKMPPTEPEC
                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7JHJO MACNE PRELIMINARY;
Q7JHJO;
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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63 GKEVRNGTPEFRGRLAPLASSRFLHD------HQAELHIRDVRGHDASIYVCRVEVL 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 ---GLGVGTGNGTRLVVEKEHPQLGAGTVLLLRA----GFYAVSFLSVAVGSTVYYQGKC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 WMLLLILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVP
                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%; Score 119; DB 2; Length 223; 26.7%; Pred. No. 0.044; tive 25; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                               1 37 Potential.
223 AA; 24683 MW; BDE42248A00398FA CRC64;
                     GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR008099; CTLA4.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
PRINTS; PR01720; CTLANTIGEN4.
SWART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 LTWKGPRRQLPAVVPAPLPPPC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 LKKRSPLTTGVYVKMPPTEPEC 211
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Interpro; IPR003596; Ig v.
PRINTS; PR01720; CTLANTIGEN4.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBDC4_MACMU PRELIMINARY;
Q9BDC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 26.7
hes 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
      SMR; Q7JHJ2; 37-161.
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SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                       Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 VTEVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 ---GLGVGTGNGTRLVVEKEHPQLGAGTVLLLRA----GFYAVSFLSVAVGSTVYYQGKC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                   MEDLINE=11393618 PubMed=11491535; DOI=10.1007/s002510100322;
A Vilinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
A Willinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
A Willinger F., Ansaria A.A.;
A Willinger F. and A.B.;
A Colonia, Sale and Co-stimulatory molecules.";
A Bas-ligand and Co-stimulatory molec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Sukrayyota w Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Barchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecines; Cercocebus.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDLINE=21383618; PubMed=11491535; DOI=10.1007/8002510100322; Villinger P., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.N. and homology analysis of nonhuman primate "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-1igand and co-stimulatory molecules."; Immunospenetics 53:315-328(2001). EMBL; AF344481; AAK37608.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%; Score 119; DB 2; Length 223; 26.7%; Pred. No. 0.044; tive 25; Mismatches 95; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 37 Potential.
223 AA; 24683 MW; BDE42248A00398FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7JHJ2_CERTO PRELIMINARY;
Q7JHJ2;
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                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                   NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
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Matches
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001). EMBL; AF346846; AAK37605.1; -; mRNA. HSSP; P16410; 1185. SWR; Q9BDC4; 37-161. GO; G0:0016021; Cintegral to membrane; IEA. GO; G0:0016020; C:embrane; IEA. GO; G0:0016020; C:embrane; IEA. GO; G0:0016020; C:embrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21383618; Pubmed=11491535; DOI=10.1007/8002510100322; Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
BDE42248A00398FA CRC64;
                                                    01-070-2001 (TrEMBLrel. 17, Created)
01-070-2001 (TrEMBLrel. 17, Last sequence update)
01-070-2003 (TrEMBLrel. 25, Last annotation update)
01-052-2003 (precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.2%; Score 119; DB 2; 26.7%; Pred. No. 0.044;
223 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Search completed: February 27, 2006, 18:03:03 Job time: 233 secs

4, Appli 3709, Ap 2, Appli

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Sequence
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Sequence
                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08228208A
Patent No. 6090914
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Linsley, Peter S.
APPLICANT: Brady, William
APPLICANT: Brady, William
APPLICANT: Wallace, Philip M.
TITLE OF INVENTION: CTLA4/CD281G HYBRID FUSION
TITLE OF INVENTION: PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B: Merchant & Gould
11150 Santa Monica Boulevard, Suite 400
US-09-227-595-30
US-08-595-590B-32
US-08-595-590B-32
US-08-1010-104-13709
US-01-104-047-3709
US-09-471-276-855
US-09-471-276-855
US-09-227-595-24
US-09-227-595-26
US-09-227-595-26
US-09-227-595-28
US-09-227-595-28
US-09-227-595-28
US-08-595-590B-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,470
FP: 30436-30US01
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTEND VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,208A
FILING DATE: 15-APR-1994
CLASSIFICATION: 435
FRICK APPLICATION DATA:
APPLICATION NUMBER: 08/008,898
FILING DATE: 22-JUN-1993
APPLICATION NUMBER: 07/723,617
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Adriano, Sarah B
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 3043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
TELEPHAX: 310 445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTR: 21P: 90025
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-228-208A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Los Angeles
CA
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STATE:
  Sequence 17, Appl
Sequence 11449, A
Sequence 1, Appl
Sequence 6602, Ap
Sequence 2, Appl
Sequence 7589, Ap
Sequence 7580, Ap
Sequence 47, Appl
Sequence 47, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, App]
                                                                                           February 27, 2006, 18:03:18; Search time 47 Seconds (without alignments) 353.570 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 100,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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Sequence 1
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Sequence 3
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Sequence 1
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1 MAWMLLLILIMWHPGSCALW.....APLPPPCGSSAHLLPPVPGG
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               version 5.1.7
- 2006 Biocceleration Ltd
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.: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

?: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

/ cgn2_6/ptodata/1/iaa/H_COMB.pep:*

/ cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

/ cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

/ cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-454-651B-17

US-09-957-688C-11449

US-09-957-688C-2

US-09-957-688C-2

US-09-957-688C-2

US-09-949-016-7589

US-09-949-016-7589

US-09-949-016-7589

US-09-646-561-42

US-09-646-561-42

US-09-646-561-42

US-08-68-889-14

US-08-889-666-14

US-08-889-666-14

US-08-4889-666-14

US-08-488-067-100

US-09-472-087-100

US-09-472-087-100
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                            572060 segs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
              GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
                                                                                                                                                 US-10-696-259-6
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Match 1
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106.5
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106
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Maximum DB R
                                                                  OM protein
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                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                            Run on:
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No.
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29;

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65 EVRNGTPEFRGRLAPLASSRFLHD------HQAELHIRDVRGHDASIYVCRVEVL-- 113
                                                                                                                                                                                                                            114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLLRA----GFYAVSFLSVAVGSTVYYQGKCLT 168
                                                                                                                                                                                                                                                                                                          6 LLILIMVHPGSC-ALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGK 64
                                                                                                                                                            24 ILFFILFIPVFCKAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRQADSQVT
                                                        Length 223;
                                                                                            Indels
                                                      11.1%; Score 118.5; DB 2; 27.0%; Pred. No. 0.00037; tive 24; Mismatches 93;
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/09957688C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 WKGPRROLPAVVPAPLPPPC 188
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                                                                                                                                                                                                                                                                                                                                                                  169 WKGPRROLPAVVPAPLPPPC 188
                                                                                                                                                                                                                                                                                                                                                                                                        192 KRSPLTTGVYVKMPPTEPEC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 27.03
Matches 54; Conservative
                                                                                                  54; Conservative
                                                                          Best Local Similarity
Matches 54; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-11449
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US-09-957-688C-1
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US-09-454-651B-17
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                                                              Query Match
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                                                                                                                                                                                                  83 EVCAAİYMMGNELT-----PLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYP 136
                                                                                                                                                                                                                                                                              137 PPYYLGIGNGTQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFLTAVSLS-----KMLK 191
                                                                                                                                                                                65 EVRNGTPEFRGRLAPLASSRFLHD------HQAELHIRDVRGHDASIYVCRVEVL-- 113
                                                                                                                                                                                                                                                        114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLLRA----GFYAVSFLSVAVGSTVYYQGKCLT 168
                                                                                                    6 LLILIMVHPGSC-ALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGK 64
                                                                                                                                          24 LLFFLLFIPVFCKAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRQADSQVT
                                                                  29;
                          Length 223;
                                                                93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wallace, Philip M.
TITLE OF INVENTION: CTLA4/CD2819 HYBRID FUSION
PROTEINS AND USES THEREOF
                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Mandel & Adriano
STREET: 35 N. Arroyo Parkway, Suite 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.30USD1
TELECOMMUNICATION INFORMATION:
                          th 11.1%; Score 118.5; DB 2 Similarity 27.0%; Pred. No. 0.00037; 54; Conservative 24; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURENTER: IBM Compacible
COMPUTER: IBM Compacible
OPERATING SYSTEM: DOS
SOFTWARE: FEBESEQU VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,651B
FILING DATE: 06-Dec-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/228,208
FILING DATE: 15-APR-1994
APPLICATION NUMBER: 08/008,898
FILING DATE: 22-JAN-1993
APPLICATION NUMBER: 01/723,617
FILING DATE: 27-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09454651B
Patent No. 6887471
GENERAL INFORMATION:
APPLICANT: Lineley, Peter S.
Ledbetter, Jeffrey A.
Damle, Witin K.
Brady, William
                                                                                                                                                                                                                                                                                                                                      169 WKGPRRQLPAVVPAPLPPPC 188
                                                                                                                                                                                                                                                                                                                                                                            192 KRSPLTTGVYVKMPPTEPEC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 223 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 626 395-7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 91103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 626 395-0694
TELEX: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Pasadena
STATE: California
COUNTRY: USA
                                Query Match
Best Local Similarity
Matches 54; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-09-454-651B-17
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92 EVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTİQGLRAMDTGLYICKVELMYP 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 PPYYLGIGNGTQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFLLTAVSLS-----KMLK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                     33 LLFFLLFIPVFCKAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRQADSQVT
                                                                                                                                                                                                                                                                                                                                                                                                           6 LLILIMVHPGSC-ALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BVRNGTPEFRGRLAPLASSRFLHD------HQAELHIRDVRGHDASIYVCRVEVL--
                                                                                                                                                                                                                                                                                                                                                   11.1%; Score 118.5; DB 2; Length 232; 27.0%; Pred. No. 0.00039; Live 24; Mismatches 93; Indels 29
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24 LLFFLLFIPVFCKAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRQADSQVT 82
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LIU, YANG
APPLICANT: ZHENG, PAN
APPLICANT: LU, PING
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Best Local Similarity
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TRNGTH: 223
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                                                                                                                                 APPLICANT: LIV, PING
APPLICANT: MOSINGER, BEDRICH
APPLICANT: MOSINGER, BEDRICH
APPLICANT: MOSINGER, BEDRICH
APPLICANT: MOSINGER, BEDRICH
TITLE OF INVENTION: CTLA4 SIGNALING
TITLE OF INVENTION: CTLA4 SIGNALING
TITLE OF INVENTION: CTLA4 SIGNALING
TITLE REPREBENCE: 227277/04025
CURRENT APPLICATION NUMBER: 00/234,089
PRIOR APPLICATION NUMBER: 60/234,089
PRIOR PILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/2414
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PAPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION UNMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 PYFVGMGNGTQIYVIDPEPCPDSDFLLWILVAVSLGLFFYSFLVTAVSLS-----KMLKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 GLGVGTGNGTRLVVEKEHPQLGAGTVL----LLRAGFYAVSFLSVAVGSTVYYQGKCLTW 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: || |: | |: || |: || |: || |: || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 117; DB 2;
; Pred. No. 0.00053;
28; Mismatches 97
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 26.1%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
                                                                                                      ZHENG, PAN
                           GENERAL INFORMATION:
APPLICANT: LIU, YANG
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US-09-949-016-6602
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LENGTH: 223
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LENGTH: 223
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APPLICANT: MOSINGER, BEDRICH
APPLICANT: MAY, KEN
TITLE OF INVENTION: ANIMAL MODEL FOR IDENTIFYING AGENTS THAT INHIBIT OR ENHANCE
TITLE OF INVENTION: CTLA4 SIGNALING
FILE REPERBYCE: 22727/04025
CURRENT APPLICATION NUMBER: U5/09/957,688C
CURRENT FILING DATE: 2001-09-20
PRIOR PILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VERSION 3.2
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                                    114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLLRA----GFYAVSFLSVAVGSTVYYQGKCLT 168
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                                                                                                                                                   EVRNGTPEFRGRLAPLASSRFLHD------HQAELHIRDVRGHDASIYVCRVEVL-- 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 10.9%; Score 116.5; DB 2; Length 3 Similarity 27.0%; Pred. No. 0.0006; 54; Conservative 24; Mismatches 93; Indels
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Patent No. 6534482
GENERAL INPORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Bermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
                                                                                                                                                                                                                              169 WKGPRRQLPAVVPAPLPPPC 188
                                                                                                                                                                                                                                                                                       192 KRSPLTTGVYVKMPPTEPEC 211
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176 LPA 178
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US-09-949-016-7590
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; Sequence 7589, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: 60/241, 755
pRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR APPLICATION NUMBER: 60/231, 768
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR SPILING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GKEVRNGT--PEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 MLLLILILIMVHPGSCALWVSQ-PPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVP 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 MLLLILLIMVHPGSCALWVSQ-PPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVP 62
              TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Immune Response and Methods of Using the Same FILE REFERENCE: 399563-2002.01
CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.9%; Score 116; DB 2; Length 226; Best Local Similarity 27.3%; Pred. No. 0.00069; Matches 50; Conservative 27; Mismatches 76; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: human MB-1 Ig-alpha
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Matches 50; Conservative
Epimmune Inc
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPA 178
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-7589
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                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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Sequence 7590, Application US/09949016

; Sequence 750, Application US/09949016
; Sequence 750, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICAMY: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: 60/241, 755
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR PILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; RIOR PILING DATE: 2000-10-03
; RIOR PILING DATE: 2000-10-03
; ROPTWARE: FREEEEQ for Windows Version 4.0
; SEQ ID NO 7590
; LENGTH: 232
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121 NGTRLVVEKEHPQ----LGAGTV-LLLRAGFYAVSFLSVAVGSTVYYQGKCLTWKGPRRQ 175
                                                                                                                                             63 GKEVRNGT -- PEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 MLLLILIMVHPGSCALWVSQ-PPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVP
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APPLICANT: Sellins, Karen S.
TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-1-C1-PCT
CURRENT APPLICATION NUMBER: US/09/646,561
CURRENT FILING DATE: 2000-09-19
PRIOR PRILING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.9%; Score 116; DB 2; Best Local Similarity 27.3%; Pred. No. 0.00071; Matches 50; Conservative 27; Mismatches 76.
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78 APLASSRFLHD------HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 VVEKEHPQLGAGTVLLLRA----GFYAVSFLSVAVGSTVYYQGKCLTWKGPRRQLPAVVP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNEL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 ALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRL
                                                                                                                                                                                                                                                   APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shellon & Mak
STREET: 225 South Lake Avenue, Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.3%; Score 110; DB 1; Length 187; 26.7%; Pred. No. 0.0022; Live 22; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: APENICAL BACHOLIN Release #1.0, Version #1.25
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/067,684
FILING DATE: 26-MAY-1993
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 7848-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-08-008-898-14
; Sequence 14, Application US/08008898
; Patent No. 5770197
                                                                                                                                                     Sequence 14, Application US/08067684; Patent No. 5434131
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
             : | | | | |
193 RSPLTTGVYVKMPPTEPEC 211
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TYPE: amino acid
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Best Local Similarity 26.7%
Marches 50; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Pasadena
STATE: California
COUNTRY: U.S.A.
ZIP: 91101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 PYYVGMGNGTQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFLITAVSLS----KMLKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS, NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 VRNGTPEFRGRLAPLASSRFLHD------HQAELHIRDVRGHDASIYVCRVEVL--- 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 VRNGTPEFRGRLAPLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL--- 113
                                                                                                                                                                                                                                                                                                                                                              6 LLILIMYHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKE 65
                                                                                                                                                                                                                                                                                                                                                                                                6 LLILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKE 65
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                                                                                                                                                                                                                                                                                                             28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
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                                                                                                                                                                                                                                                        Sequence 47, Application US/09646561

Patent No. 6852847

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee;

APPLICANT: Sim, Gek-Kee;

APPLICANT: Sim, Gek-Kee;

TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PR;

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF;

FILE REFERENCE: IM-1-C1-PCT

CURRENT APPLICATION NUMBER: 08/09/646,561

CURRENT FILING DATE: 1998-03-19

PRIOR FILING DATE: 1998-03-19

PRIOR FILING DATE: 1998-03-19

PRIOR FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PATENTIN VOICE ST
PRIOR APPLICATION NUMBER: 09/062,597
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 42
LENGTH: 223
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 RSPLTTGVYVKMPPTEPEC 211
                                                                                                                                                                               ; ORGANISM: Canis familiaris US-09-646-561-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Felis catus
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 52; Conserv
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LENGTH: 223
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TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-459-818-14
      CORRESPONDENCE ADDRESS:
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STATE: California
COUNTRY: USA
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                  APPLICANT: Linsley, Peter S
APPLICANT: Ledbetter, Jeffrey A
APPLICANT: Demle, Nitin K
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.3%; Score 110; DB 1; Length 187; 26.7%; Pred. No. 0.0022; Live 22; Mismatches 87; Indels
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Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                             COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,898
                                                                                                                                                            E: Sheldon & Mak
201 South Lake Avenue, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/723,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MATGAL
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 7848
TELECPHONE: (818) 796-4010
TELEPHONE: (818) 796-4010
TELEFRA: (818) 796-6321
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 187 amino acids
amino acid
                                                                                                                                                                                               CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91101
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Best Local Similarity
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GENERAL INFORMATION:
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CITY: Load Angeles

CONTINES: California

CONTINES: California

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MEDIUM TYPE: Floppy disk

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MEDIUM TYPE: Floppy disk

CONTINES BLANAME PORM:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.3%; Score 110; DB 1; Length 187; Best Local Similarity 26.7%; Pred. No. 0.0022; Matches 50; Conservative 22; Mismatches 87; Indels 28; Gaps
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-JUL-1997
CLASSIFICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION NUMBER: 34,470
FILING DATE: Adriano, Sarah B.
NAME: Adriano, Sarah B.
REGISTMATION NUMBER: 34,470
TELECOMMUNICATION INFORMATION:
TELEPRATION NUMBER: 31,470
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-889-666-14
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21, Appl 316, App 86, Appl 1, Appli 32, Appl 32, Appl 32, Appl 32, Appl

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Sequence 6, Application US/10696259;
Publication No. US20040110218A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC
APPLICANT: BIOGEN, INC
TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Pamily and Its Use for TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Pamily and Its Use for INVENTION: Myelin-Oligodendrocyte Glycoprotein Pamily and Its Use for INVENTION: Myelin-Oligodendrocyte Glycoprotein Pamily and Its Use for FILE REFRENCE: A041 US
FILE REFRENCE: A041 US
CURRENT PILING DATE: 2003-10-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-07
NUMBER OF SEQ ID NOS: 20
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 201
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US-11-052-559-1

US-09-989-545-21

US-09-928-267-21

US-10-225-519-8

US-10-207-655-101

US-10-491-997-76

US-11-120-777-21

US-11-120-777-21

US-10-207-655-316

US-10-207-655-316

US-10-207-65-316

US-10-371-669-32

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; ORGANISM: Homo sapien
US-10-696-259-6
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           US-10-696-259-6
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Sequence 17,
Sequence 12,
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Sequence 9, 1
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Sequence 4, 1
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cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US11_FUBCOMB.pep:*
                                         GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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US-10-696-259-9

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US-10-333-481-17

US-10-381-444-4

US-10-381-137-649-4

US-10-396-359-8

US-10-381-137-649-4

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US-10-155-514-2

US-10-155-514-2

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US-10-165-644-6

US-10-165-644-6

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US-10-165-644-6

US-10-161-148-6

US-10-17-100-17-100-17-100-17-100-17-100-17-100-17-100-17-100-17-100-17-100-17-100-17-100-18-100-17-100-17-100-17-100-18-100-18-100-17-100-18-100-18-100-17-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-100-18-
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Match Length
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                                      Mismatches
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Best Local Similarity 89.2%;
Matches 173; Conservative
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                                   Conservative
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                               Matches 173;
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Publication No. US20020142445A1

GENERAL INFORMATION:

APPLICANT: INFORMATION:

APPLICANT: UNIVERSITA DI GENOVA

ITILE OF INVENTION: Cytocoxicity mediated by human Natural Killer cells and

ITILE OF INVENTION: antibodies that identify the same"

CURRENT APPLICATION NUMBER: US/10/036,444

CURRENT FILING DATE: 1999-11-15

PRIOR FILING DATE: 1999-11-15

PRIOR FILING DATE: 1999-11-15

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1
                                                                                                   APPLICANT: BIOGEN, INC
APPLICANT: BIOGEN, INC
APPLICANT: BIOGEN, INC
APPLICANT: BIOGEN, INC
TITLE OF INVENTION: BMOG, A Novel Protein Member of the
TITLE OF INVENTION: BMOG, A Novel Protein Member of the
TITLE OF INVENTION: Immunomodulatory Purposes
TITLE OF INVENTION: Immunomodulatory Purposes
FILE REPERENCE: A041 US
CURRENT APPLICATION NUMBER: US/10/696,259
CURRENT FILING DATE: 2000-40-28
PRIOR FILING DATE: 2000-40-28
PRIOR FILING DATE: 1998-11-05
PRIOR PILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-07
NUMBER OF SEC ID NOS: 20
SOFTWARE: FastSEC for Windows Version 4.0
SEC ID NOS: 20
SEC ID NOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.4%; Score 1017.5; DB 4; Length 198; 98.0%; Pred. No. 1.1e-86; ive 0; Mismatches 1; Indels 3;
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Pred. No. 1.7e-73;
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Sequence 9, Application US/10696259 Publication No. US20040110218A1 GENERAL INFORMATION:
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89.2%;
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Best Local Similarity 98.0
Matches 197; Conservative
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US-10-036-444-2
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; ORGANISM: Homo sapien
US-10-696-259-9
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US-10-036-444-2
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JOHNSTON THE NOTE AND A PEPLICANT: BIOGEN, INC
APPLICANT: BROWNING, Jeffrey
TITLE OF INVENTION: BMOG, A Novel Protein Member of the
TITLE OF INVENTION: BMOG, A Novel Protein Member of the
TITLE OF INVENTION: Immunomodulatory Purposes
TITLE OF INVENTION: Immunomodulatory Purposes
TITLE OF INVENTION: Immunomodulatory Purposes
TITLE OF INVENTION: Immunomodulatory Purposes
CURRENT PEPLICATION NUMBER: US/10/696,259
CURRENT FILING DATE: 2003-10-28
PRIOR APPLICATION NUMBER: PCT/US98/23826
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FREUENCE FOR WINDOWS VETSION 4.0
SEQ ID NO 4
SEQ ID NO 4
                                                                                 61 VPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
                                                                                                                                                          121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGK------CLTWKGP 172
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US-11-137-649-2
US-11-137-649-2
; Sequence 2, Application US/11137649
; Publication No. US20050221438A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
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1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEV
                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 7, Application US/10696259; Publication No. US20040110218A1; GENERAL INFORMATION:
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Best Local Similarity 89.8
Matches 168; Conservative
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US-10-696-259-7
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179 IPEPRCP 185
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APPLICANT: BIOGEN, INC
APPLICANT: BROWNING, Jeffrey
TITLE OF INVENTION: BMCG, A Novel Protein Member of the
TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for INVENTION: Immunomodulatory Purposes
FILE REPRENCE: A041 US
CURRENT APPLICATION NUMBER: US/10/696,259
CURRENT FILING DATE: 2000-10-28
PRIOR APPLICATION NUMBER: PCT/US98/23826
PRIOR APPLICATION NUMBER: PCT/US98/23826
PRIOR APPLICATION NUMBER: PCT/US98/23826
PRIOR APPLICATION NUMBER: PCT/US98/23826
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PRIOR APPLICATION NUMBER: PCT/US98/23826
PRIOR APPLICATION NUMBER: PCT/US98/23826
PRIOR APPLICATION NUMBER: PCT/US98/23826
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASTEEQ for Windows Version 4.0
### APPLICANT: UNIVERSITA DI GENOVA
### TITLE OF INVENTION: "Novel triggering receptor involved in natural
### TITLE OF INVENTION: "Voctoxizity mediated by human Natural Killer cells and
### TITLE OF INVENTION: antibodies that identify the same"
### TITLE OF INVENTION: antibodies that identify the same"
### TITLE OF INVENTION: Antibodies that identify the same"
### FILE REFERENCE: SEQ-FR-1060
### CURRENT PAPLICATION NUMBER: US/11/137,649
### PRIOR FILING DATE: 2002-01-07
### PRIOR FILING DATE: 1099-11-15
### PRIOR FILING DATE: 1999-11-15
### PRIOR FILING DATE: 1999-11-15
### PRIOR FILING DATE: 1999-12-07
### NUMBER OF SEQ ID NOS: 13
### SEQ ID NO 2
### LENGTH: 190
### LENGTH: 190
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### LENGTH: 190
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Best Local Similarity 89.2
Matches 173; Conservative
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US-10-696-259-5
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APPLICANT: BICKEN, INC
APPLICANT: BICKEN, INC
APPLICANT: BROWNING, Jeffrey
TITLE OF INVENTION: BMOG, A Novel Protein Member of the
TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
TITLE OF INVENTION: Immunomodulatory Purposes
FILE REFERENCE: A041 US
CURRENT APPLICATION NUMBER: US/10/696,259
CURRENT PILING DATE: 2003-10-28
PRIOR APPLICATION NUMBER: BC/US98/23826
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-07
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
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Publication No. US20040110218A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BROWNING, Jeffrey
TITLE OF INVENTION: BWOG, A Novel Protein Member of the
TITLE OF INVENTION: Immunomodulatory Purposes
FILE REFERENCE: A041 US
CURRENT APPLICATION NUMBER: US/10/696,259
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                                   1 MAWMLLILILIMVHPGSCALMVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEV
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us-10-696-259-6.rapbm

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119 NGTRLVVBKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYHGK 163
                                                                                                 ; Sequence 17, Application US/10333481; Publication No. US20040072256A1; GENERAL INFORMATION:
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Best Local Similarity 100.C
Matches 135; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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US-10-333-481-17
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US-10-333-481-18
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LENGTH: 369
TYPE: PRT
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APPLICANT: BROWNING, Jeffrey
APPLICANT: BROWNING, Jeffrey
APPLICANT: BROWNING, Jefrey
TITLE OF INVENTION: BMGG, A Novel Protein Member of the
TITLE OF INVENTION: Immunomodulatory Purposes
TITLE OF INVENTION: Immunomodulatory Purposes
TITLE OF INVENTION: Immunomodulatory Purposes
TITLE OF INVENTION: Immunomodulatory Purposes
CURRENT APPLICATION NUMBER: US/10/696,259
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US/09/560,85A
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-07
NUMBER: OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VPGKEVRNGTPEFRGRLAPLASSRFLHDHQABLHIRDVRGHDASIYVCRVEVLGLGVGTG 120
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                                                                                                                                                                                                                                                                                                                                                 0; Indels
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98.2%; Pred. No. 8.7e-69;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
          PRIOR APPLICATION NUMBER: US/09/560,855A
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 1900-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR PILING DATE: 1997-11-07
PRIOR PILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PRECEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/10696259; Publication No. US20040110218A1; GENERAL INFORMATION:
2003-10-28
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.4 Matches 161; Conservative
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Best Local Similarity 98.2
Matches 162; Conservative
                                                                                                                                                                                                                       type: PRT CORGANISM: Homo sapien US-10-696-259-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Homo sapien
US-10-696-259-8
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-696-259-8
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                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: Ofer Mandelboim
APPLICANT: Angel Porgador
TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSITY
TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSITY
FILE REFERENCE: 68657
CURRENT APPLICATION NUMBER: US/10/33,481
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: PCT/IL01/00664
PRIOR APPLICATION NUMBER: PCT/IL01/00664
PRIOR FILING DATE: 2001-07-19
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 17
LENGTH: 135
TYPE: PRT
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Publication No. US20040072256A1

Publication No. US20040072256A1

Publication No. US20040072256A1

APPLICANT: Ofer Mandelboim

APPLICANT: Angel Porgador

TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSITY

FILE REPERENCE: 68657

CURRENT APPLICATION NUMBER: US/10/333,481

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: PCT/IL01/00664
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Pred. No. 1.8e-58;
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Sequence 49, Application US/0909567B

Publication No. US20030022257A1

GENERAL INFORMATION:

APPLICANT: Macina, Roberto A.

APPLICANT: Mair, Manoj

APPLICANT: Chen, Seiyu

TITE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes

FILE REFERENCE: DATE: 2001-07-20

CURRENT APPLICATION NUMBER: US/09/909,567B

CURRENT FILING DATE: 2001-07-21

NUMBER OF SEQ ID NOS: 56

SEQ ID NOS: 56

LENGTH: 246
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Publication No. US20030083246A1

GENERAL INFORMATION:
APPLICANT: Carr, Suzette
APPLICANT: Hagerty, David
APPLICANT: Becker, Jean-Claude
APPLICANT: Becker, Jean-Claude
APPLICANT: Becker, Jean-Claude
TITLE OF INVENTION: CTLA4 MOLECULE
TITLE OF INVENTION: CTLA4 MOLECULE
FILE REFERENCE: D0030NP/30436.55USIN
CURRENT APPLICATION NUMBER: US/09/898,195A
CURRENT APPLICATION NUMBER: US/02-04-15
PRIOR APPLICATION NUMBER: 60/215,913
PRIOR FILING DATE: 2000-07-03
                                                                                                                                                                                                                                                        61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
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                                                                       19 LWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLA
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0; Gaps
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   0; Indels
   0; Mismatches
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SOFTWARE: Patentin Ver. 2.1
120; Conservative
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ORGANISM: Homo sapien
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US-09-909-567B-49
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Best Local
   Matches
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                                                                                                                                                                                                                                                            Sequence 4, Application US/10036444

Publication No. US2002014245A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENT
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Publication No. US20050221438A1

GENERAL INPORMATION

APPLICANT: INNATE PHARMA S.A.S.

APPLICANT: UNIVERSITA DI GENOVA

TITLE OF INVENTION: "Novel triggering receptor involved in natural

TITLE OF INVENTION: "Octooxicity mediated by human Natural Killer cells and

TITLE OF INVENTION: antibodies that identify the same"

FRICH REPRENCE: SEQ-FR-1060

CURRENT APPLICATION NUMBER: US/11/137,649

FRIOR FILING DATE: 1099-11-15

PRIOR FILING DATE: 1999-11-15

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

LENGTH: 120
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                                                                       NGTRLVVEKEHPOLG 135
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ORGANISM: Human NK cell
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Best Local Similarity
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US-10-036-444-4
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223
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US-10-866-120-8
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Sequence 1, Appli
Sequence 3709, Ap
Sequence 1015, Ap
Sequence 248, App
Sequence 248, App
Sequence 1545, Ap
Sequence 1545, Ap
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815, App
62, Appl
877, App
66, Appl
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70, Appl
69, Appl
63, Appl
67, Appl
64, Appl
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4, Appli
                                                                                                   February 27, 2006, 18:04:53 ; Search time 19 Seconds (without alignments) 157.491 Million cell updates/sec
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US-11-128-900-100

US-11-128-440-9

US-11-072-512-3709

US-11-072-512-3709

US-11-072-512-3709

US-11-072-512-3233

US-11-072-512-3233

US-11-072-512-3233

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US-11-072-512-3233

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US-11-052-186-66

US-11-062-186-69

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Maximum Match 100%
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Sequence 8, Application US/10866120

Sequence 8, Application US/10866120

Sequence 8, Application No. US20050277173A1

Sequence 8, Application No. US20050277173A1

SEQUENCE 8, APPLICANT: Halv. Shu-Ching

APPLICANT: Chin, Li-Te

APPLICANT: Halv. Shu-Ching

TITLE OF INVENTION: INVERSE AGONIST

TITLE OF INVENTION: INVERSE AGONIST

TITLE OF INVENTION: INVERSE US/10/866,120

CURRENT APPLICATION NUMBER: US/10/866,120

CURRENT APPLICATION NUMBER: US/10/866,120

CURRENT APPLICATION NUMBER: US/10/866,120

SCURRENT PILING DATE: 2004-06-14

SEQ ID NOS: 8

SEQ ID NO 8
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  2070, Ap
1484, Ap
108, App
108, App
107, Ap
107, Ap
1570, Ap
1564, Ap
1574, Ap
115, App
412, App
416, App
416, App
418, App
418, App
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418, App
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                                                                                                                                                                                                 127, App
9, Appli
4, Appli
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Sequence 126, App
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                                     Sequence 1
Sequence 1
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US-11-054-515-2070
US-11-000-453-755
US-11-080-991-108
US-11-084-515-1207
US-11-054-515-1207
US-11-054-515-1207
US-11-054-515-1570
US-11-054-515-1564
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US-11-054-515-1564
US-11-054-517-127
US-11-055-877-127
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US-11-087-177-9
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                                                                                                                                                                                                                                                                            ALIGNMENTS
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEX: PEPTIDE
LOCATION: (1) .. (223)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2004-03-15
RELEVANT RESIDUES: (1) .. (223)
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2532
2532
2532
2550
11700
17700
17700
281
281
3054
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Best Local Similarity
Matches 54; Conserval
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Length 364;

Indels

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4 MILLILIMWHP--GSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVV 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 L---GLGVGTGNGTRLVVEKEHP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/11057923 Publication No. US20050287152A1 GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 100
LENGTH: 364
                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-11-128-900-100
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ORGANISM: Homo sapiens
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                                                                                                GENERAL INVARIATION.

APPLICANT: AMGEN INC.

APPLICANT: AFAGE, Sanjay D.

APPLICANT: Faige, Ulrich

TITLE_OF INVENTION: COMPOSITIONS AND METHODS TO MODULATE AN IMMUNE RESPONSE TO AN

TITLE_OF INVENTION: COMPOSITIONS THERAPEUTIC AGENT

FILE REFERENCE: 54113.8008.WOOD

CURRENT PELLING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: PCT/US04/35415

PRIOR APPLICATION NUMBER: DCT/US04/35415

PRIOR APPLICATION NUMBER: US 60/515,199

PRIOR PILLING DATE: 2003-10-27

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 4

LENGTH: 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 GLGVGTGNGTRLVVEKEHPQLGAGTVL----LLRAGFYAVSFLSVAVGSTVYYQGKCLTW 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 PYFVGMGNGTQIYVIDPEPCPDSDFLLWILVAVSLGLFFYSFLVSAVSLS-----KMLKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 FVALLITLFIPVFSEAIQVTQPSVVLASSHGVASFPCEYSPSHNTDEV-RVTVLRQTNDQ 80
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APPLICANT: NEVEU, MARK J.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REPERENCE: ABX-PF1 DIV3
CURRENT APPLICATION NUMBER: US 10/776649
PRIOR APPLICATION NUMBER: US 10/776649
PRIOR APPLICATION NUMBER: US 00/612497
PRIOR APPLICATION NUMBER: US 00/612497
PRIOR APPLICATION NUMBER: US 09/472087
PRIOR PILING DATE: 1999-112-23
PRIOR FILING DATE: 1998-112-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.8%; Score 115; DB 7; Length 223; Best Local Similarity 26.1%; Pred. No. 0.0012; Matches 52; Conservative 28; Mismatches 97; Indels
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US-11-128-900-100
US-11-128-900-100, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
                                        ; Sequence 4, Application US/11057923
; Publication No. US20050287152A1
; GENERAL INFORMATION:
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OTHER INFORMATION: Murine CTLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-057-923-4
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APPLICANT: AMGEN INC.
APPLICANT: KARE, Sanjay D.
APPLICANT: Feige, Ulrich
TITLE OF INVENTION: COMPOSITIONS AND METHODS TO MODULATE AN IMMUNE RESPONSE TO AN
TITLE OF INVENTION: IMMUNGGRIC THERAPEUTIC AGENT
FILLE REFERENCE: 54113.6006.W000
CURRENT APPLICATION NUMBER: US/11/657,923
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: US 60/515,199
PRIOR PILING DATE: 2004-10-26
PRIOR FILING DATE: 2003-10-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.3
SQCIWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ----PLDDSICTGTSSGNQVNLTIQGLRAMDTGLXICKVELMYPPPYXLGIGNGTQ1YVI 115
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                                   62 PGKEVRNGTPEFRGRLAPLASSRFLHD------HQAELHIRDVRGHDASIYVCRVEV 112
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NAME/KEY: MISC PEATURE
OTHER INFORMATION: Full-lenth human CTLA-4 amino acid sequence
US-11-057-923-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
9.9%; Score 106; DB 7; Length 186;
Best Local Similarity 26.6%; Pred. No. 0.0066;
Matches 49; Conservative 21; Mismatches 86; Indels
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159 GKTRLVVQVPPVIENGLPDLSTTEGSHAFLPCKARGSPE----PNITWDKD----- 205
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Best Local Similarity 29.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 NGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 9.7%; Score 103.5; DB 7;
1 Similarity 27.9%; Pred. No. 0.022;
29; Conservative 11; Mismatches 37;
                          APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MAGAHARI, KENJI
APPLICANT: MAGAHARI, KENJI
APPLICANT: MAGAHARI, KENJI
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US (11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 2001-379298
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SEQ ID NOS: 4096
SEQ ID NOS: 4096
SEQ ID NOS: 201
YOSHIKAWA, TSUTOMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3709
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; ORGANISM: Homo sapiens
US-11-054-515-1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 IGAGTVLLLRAGFYAVSFLSVAVGSTVYYQGKCLTWKGPRRQLPAVVPAPLPPP----C 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 WGQGT------QVTVSSE-----PVKTPKPQPQPQPQPDPTTESKC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 D------HQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 DSVKGRFTISRDNAKNTMYLOMNSMKAEDTAVYYCAAD----SDYGPGRR---SSEYDY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 GSSAFLPCSFNASQGR----LAIGSVTWFRDEVVPGKEVRNGTPEFRGRLAPLASSRFLH 87
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Law, Chel-Leung
APPLICANT: Law, Chel-Leung
APPLICANT: Daw, Chel-Leung
APPLICANT: Daw, Raj
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
TITLE OF INVENTION: LYMHHOCYTE ACTIVATION
FILE REFERENCE: 980034.408D1
CURRENT APPLICATION NUMBER: US/11/128,440
CURRENT FILING DATE: 2005-05-12
PRIOR FILING DATE: 2003-08-21
PRIOR PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 09/252,150
PRIOR APPLICATION NUMBER: US 09/252,150
PRIOR PILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 80
SOFTWARE FEASTER OF WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.8%; Score 105; DB 7; Length 205; Best Local Similarity 24.9%; Pred. No. 0.0091; Matches 50; Conservative 15; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3709, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                           APPLICANT: Ledbetter, Jeffrey A. APPLICANT: Hayden-Ledbetter, Martha APPLICANT: Brady, William A. APPLICANT: Grosmaire, Laura S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 ----- GSSAHLLPPVP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 PKRPAPELLGGPSVFIFPPKP 168
                                                                                                   Sequence 9, Application US/11128440 Publication No. US20050261478A1 GENERAL INFORMATION:
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHIN, SHIZUKO
APPLICANT: ISHIN, YURI
APPLICANT: HOW, YURI
APPLICANT: HOW, YURI
APPLICANT: HOW, YURI
APPLICANT: HOW, YURI
APPLICANT: TRIER: RYOTARO
APPLICANT: IRIER: RYOTARO
APPLICANT: TRIER: RYOTARO
APPLICANT: SEKI, NAOHIKO
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                                                             -11-128-440-9
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9
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                                                                                                                                       195 NRPSGVP---GRFSGSKSGT----SASLAITGLQAEDEADYYCQSYDNSLNGVLFGGGT 246
                                                           139 GSAQSVVTQPPSVSAAPGQRVTISCS--GSSSNIGINSVSWYQQ--LPGKAPKLLIYNNS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AWMLLLILIMWHPGSCALWVSQPPEIRTLE-GSSAFLPCSFNASQGRLAIGSVTWFRDEV 60
                                                                                                             ---NGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGL-GVGTGNGT 123
                                     67
                                                                                                                                                                                                                                                                                                                         Sequence 1015, Application US/10821234
; Publication No. US2005025114A1
; Publication No. US2005025114A1
; GENERAL INPORMATION:
   APPLICANT: Labat, Ivan
; APPLICANT: Adarmani, Susan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT FILING DATE: 2004-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
                                     15 GSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVR-----
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73; Indels
49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Cao, Y1-Cheng
APPLICANT: Drmanac, Radeng
APPLICANT: Drmanac, Radeng
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 IYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVL 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.5%; Score 101.5; DB
Best Local Similarity 25.6%; Pred. No. 0.062;
Matches 40; Conservative 16; Mismatches 7
   16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 248, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1015
LENGTH: 555
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rul-hong
APPLICANT: Qian, Xiaohong
   36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang, Zhiwei
Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1015
                                                                                                                                                                                             124 RLW 127
                                                                                                                                                                                                                               247 QLTV 250
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US-10-821-234-1015
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   Matches
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58 YPSWHQQ--TPGQPPR--TLIYNTHIRASGVSDRFSGSIVGNKAALTITGAQADDECVYY 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAWMLLLILIMVHPGS----CALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIGSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.2%; Score 98; DB 7; Length 240;
Best Local Similarity 25.0%; Pred. No. 0.049;
Matches 54; Conservative 26; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFLSVAVGSTVYYQGKCLTWKGPRRQLPAVVPAPLP 185
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                                                 CURKENN FILLING DATE: 2003-11-23
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
PRIOR PILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-02-25
PRIOR FILING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-35
PRIOR PILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-15
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APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVIKI
APPLICANT: NAGHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVel full length CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-07
PRIOR APPLICATION NUMBER: US 60/350,978
CURRENT APPLICATION NUMBER: US/11/000,463
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISHII, SHIZUKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-000-463-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-072-512-3233
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APPLICANT:
APPLICANT:
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--GNGTRLVV 127
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242 VFGAGTKLTV 251
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APPLICANT: HANNA, PETER
APPLICANT: HANNA, PETER
APPLICANT: HANNA, PETER
TITLE OF INVENTION: CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
TITLE OF INVENTION: CC-STIMULATORY ANTIGENS
TITLE OF INVENTION: CC-STIMULATORY ANTIGENS
TITLE OF INVENTION: CC-STIMULATORY ANTIGENS
TITLE OF INVENTION: CC-STIMULATORY ANTIGENS
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TITLE OF INVENTION: CC-STIMULATORY ANTIGENS
TITLE OF INVENTION: CC-STIMULATORY ANTIGENS
TITLE OF INVENTION: CC-STIMULATORY ANTIGENS
THOR RELIGING DATE: 1995-11-08
PRIOR FILLING DATE: 1995-11-08
PRIOR FILLING DATE: 1995-06-07
NUMBER: OF SEQ ID NOS: 12
CC-STIMULATORY ANTIGENS
TO SOFTWARE: PATENTING VET. 2.1
                                                                                                                                                                                                                                                                                                                 Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 ELHIRDVRGHDASIYVCRV--EVLGLGV-----GTGN------GTRLVVEKEHP 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 TSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGDL 218
                                                                                                                                                                                                                                                                                                                                                                                                 7 WILLVAVIKGVQCEVQILESGGGLVQPGGSLTLSCAASGFIFSNYVMTWVRQAPG-KGLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 WVSS-----TAASGANTFYADSV------KGR---FTVSRDNSENMM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                               32 GSSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLAPLASSRFLHDHQA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 YTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPS--TPPTP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 -----AVGSTVYYQGKCLT----WKGPRRQLPAVVPAPLPPPCGSSAHLLPPVP
                                                                                                                                                                                                                                                                                                            78; Indels 130;
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                                                                                                                                                                                                                                                                DB 7; Length 508;
                                                                                                                                                                                                                                                         9.2%; Score 98; DB 7;
21.2%; Pred. No. 0.12;
tive 26; Mismatches
                               2001-379298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/11139499
Publication No. US200502602605A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, DARRELL R.
PRIOR FILING DATE: 2002-01-25
PRIOR PELLING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 3233
LENGTH: 508
                                                                                                                                                                                                                                                                                                                                                        3 WMLLLILI-----
                                                                                                                                                                                                                                                                                                          63; Conservative
                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3233
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Matches 63; Conserv
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LENGTH: 234
TYPE: PRT
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US-11-139-499-2
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5 LLLILIMVHPGS-CALWVSQPPEIRTLEGSSAPLPCSFNASQGRLAIGSVTWFRDE----

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109 ------RVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVLLLRAGFY--AVSFLSVAV 156
                                                                                                                                                                                                                                                                                                    60 ----VVPGKEVRNGTPE-FRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVC---- 108
                                                                                                                                                             63 PILVIYDDSDRPSGIPERFSGSKS-----GNTATLINGVEAGDEADYYCQVWDRA 113
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GENERAL INVENTALION:

TILLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFREENCE: PF523P3
CURRENT APPLICATION WIMBER: US/11/054,515
CURRENT PILING DATE: 2005-02-10
PRIOR APPLICATION WIMBER: 60/580,347
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
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8.9%; Score 95; DB 7; Length 253;
Best Local Similarity 25.4%; Pred. No. 0.098;
Matches 33; Conservative 20; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     157 GSTVYYQGKCLTWKGPRRQLPAVVPAPLP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------VAWKADSSPVKAGVETTTP 186
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NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1545, Application US/11054515; Publication No. US20050255532A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-000-463-815; Application US/11000463
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ORGANISM: Homo sapiens
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US-11-062-186-62
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55 QLKPGQSPLVVIHQDTKRPSGIPERFSGSNS------GNTATLTISGTQAMDEADYY 105
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Publication No. US20050272097A1
GENERAL INFORMATION:
APPLICANT: CALENOFF, EMANUEL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
TITLE OF INVENTION: AUTOIMMUNE DISEASES
FILE REFERENCE: 21417-98470
CURRENT APPLICATION NUMBER: US/11/062,186
CURRENT APPLICATION NUMBER: US/11/062,186
PRIOR APPLICATION NUMBER: 600546,062
PRIOR PILING DATE: 2004-02-18
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                                APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong B.
APPLICANT: Chen, Rui-hong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Chou, Ping
APPLICANT: Chou, Ping
APPLICANT: Chou, Ping
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APPLICANT: Chou, Ping
APPLICANT: Chou, Ping
APPLICANT: 2004-11-29
FRIOR APPLICATION NUMBER: US/11/000,463
FRIOR PILING DATE: 2001-01-25
FRIOR PILING DATE: 2001-01-25
FRIOR APPLICATION NUMBER: 09/491,404
FRIOR APPLICATION NUMBER: 09/491,404
FRIOR APPLICATION NUMBER: 09/617,746
FRIOR PILING DATE: 2000-01-25
FRIOR FILING DATE: 2000-01-25
FRIOR APPLICATION NUMBER: 09/631,451
FRIOR APPLICATION NUMBER: 09/631,451
FRIOR APPLICATION NUMBER: 09/631,451
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FRIOR APPLICATION NUMBER: 09/631,451
FRIOR APPLICATION NUMBER: 09/631,451
FRIOR APPLICATION NUMBER: 09/631,451
FRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
FRIOR FILING DATE: 2000-09-15
FRIOR FILING DATE: 2000-09-15
FRIOR FILING DATE: 2000-09-15
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Publication No. US20050266423A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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US-11-062-186-62
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                                                                                                                                                                                                                                                                                                                                                                                                      5 LLLILILIMV---HPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIG-SVTWFRDEV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INCRMALLANT: HUMPHREYS,
APPLICANT: HUMPHREYS,
APPLICANT: WINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH -2017US01
CURRENT FILING DATE: 2005-01-1;
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2002-09-14
PRIOR PLICATION NUMBER: 09/396,813
PRIOR PLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VPGKEV----RNG-----TPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LILILIMV---HPGSCALWVSQPPEIRTLEGSSAFLPCSFNASQGRLAIG-SVTWFRDEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 LLILLLQVSSSYAGQFRVIGPRHP-IRALVGDEVELPC--RISPGKNATGMEVGWYRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VPGKEV----RNG-----TPEFRGRLAPLASSRFLHDHQAELHIRDVRGHDASIYVC-
                                                                                                                                                                                                                                                                                                                                                    55;
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                                                                                                                                                                                                                                                                                                                                                       84;
                                                                                                                                                                                                                                                                                           Query Match

8.9%; Score 94.5; DB 7;
Best Local Similarity 27.3%; Pred. No. 0.11;
Matches 62; Conservative 26; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
PRIOR APPLICATION NUMBER: 60/545,980
PRIOR FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: Patentin version 3.3
SEQ ID NO 62
LENGTH: 247
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 877, Application US/11033039; Publication No. US20060002947A1; GENERAL INFORMATION:
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Matches 62; Conservative
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Wed Mar 1 09:25:39 2006

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Search completed: February 27, 2006, 18:07:57 Job time : 20 secs



Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1. (bases I to 10.24)

2. Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altachul, S.E., Zeeberg, B., Buetow, K.H., Schafer, C.F., Bhat, N. K., Altschul, S.E., Zeeberg, B., Buetow, K.H., Schafer, C.F., Bhat, N. K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S. Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
AF031137 Homo sapi
A516006 Pan trogl
BD087743 BMOG, nov
CS032897 Sequence
CS041849 Sequence
AF031136 Homo sapi
BD087742 BMOG, nov
BV174406 sqnm71530
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Homo sapiens natural cytotoxicity triggering receptor 3, mRNA (cDNA BC052582
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AX14814158 Sequence
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AX148141 Sequence
AX1231153 Homo sapi
AF031138 Homo sapi
AF031138 Homo sapi
CR75888 Human DNA
AL929587 Human DNA
AL929587 Human DNA
CR753892 Human DNA
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AJ278389 Macaca fa
AX035215 Macaca mu
AX035214 Macaca mu
AJ554301 Macaca mu
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AR182587 Sequence
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AX778498 Sequence
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        Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-A0=Abss/ABSSMBs spool/US10656529/runat_27022006_123555_27124/app_query.fasta_1
-Q=Abss/ABSSMBs spool/US10656259/runat_27022006_123555_27124/app_query.fasta_1
-DB=GenEmbl -QFMT=fasta_p-SUFFIX=p10.rge_-MINMATCH=0.1 -LOOPCIX=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFMT=pto -NORMestv +HEAPSIZE=500 -MINIEN=0 -MAXIEN=2000000000 -HOST=abss03p
-USR=USI0696259_@GGN 1 1 7415_@runat_27022006_123555_27124 -NCPU=6 -ICPU=3
-NO WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=12
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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1 MAWMLLLILIMWHPGSCALW.....APLPPPCGSSAHLLPFVPGG 201
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                               - nucleic search, மன்ற சொடை நிற்ற நூற நூல்வி
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Contact: MGC help desk
Contact: MGC help desk
Email: Gapba-Famail.nih.gov

Ilseue Procurement: D. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Prarayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web sites http://www.nisc.nih.gov
Contact: nisc.mgc@nhgri.nih.gov
Contact: nisc.mgc@nhgri.nih.gov
Contact: N.Ayele-K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Cuan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, P.,
Maduro, Q.L., Massiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J. C.,
McDowell, J., Pearson, R., Stanttripop, S., Thomas, P.J., Tucuhman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
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QGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHD
ASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTV
YYQGKCLTWKGPRRQLPAVVPAPLPPPCGSSAHLLPFVPGG"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24475831.
Location/Qualifiers
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.W., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length phonan and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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209-.914
/gene="NCR3"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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CS032788
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Indels:
Gaps:
                                                              (1-1024)
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Location/Qualifiers
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AF031137 1061 bp mRNA linear PRI 18-NOV-1997
Homo sapiens 1C7 precursor, mRNA, alternatively spliced, complete
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                               121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu
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YYQGKCLTWKGPRRQLPAVVPAPLPPPCGSSAQLLPPVPGG"
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Submitted (13-NOV-2002) Biassoni R., Molecular Immunology, Istituto
Scientifico Tumori, Largo Rosanna Benzi 10, Genova 16132, ITALY
Location/Qualifiers
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Mammalia, Eutheria, Euarchontoglires; Primates; Catarrhini;
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                                 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal
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Characterization of natural killer receptors in chimpanzees
Unpublishes
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15 3 (bases 1 to 1061)
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16 3 (bases 1 to 1061)
17 5 Nalabolu, S.R., Raghunathan, A., Sivakamasundari, R. and Weissman, S.M. Direct Submission
18 Submitted (1997) Genetics, Yale School of Medicine, 333
19 Cedar Street, New Haven, CT 06510, USA
10 Submitted (1997) Genetics, Yale School of Medicine, 333
10 Cedar Street, New Haven, CT 06510, USA
10 Submitted (1997) Genetics, Yale School of Medicine, 333
10 Location/Qualifiers
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QGRLAIGSVTWRRDEVVPGKEVRNGTPEFRGRLAPLASSRFLHDHQAELHIRDVRGHD
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Nalabolu,S.R., Shukla,H., Nallur,G., Parimoo,S. and Weissman,S.l Genes in a 220-kb region spanning the TNF cluster in human MHC Genomics 31 (2), 215-222 (1996)
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101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
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C12N115/09, A61K48/00, A61P37/02, C07K14/47, C07K16/18, C07K19/00,
C12N1/15,
C12N1/15,
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novel member of myelin oligodendroglia glycoprotein CC
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                                                               Location/Qualifiers
1. .834
/organism='Homo sapiens (human)'.
                                              family, and utilization thereof for immunomodulation Key
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu
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JP 2001522589-A/3
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06-NOV-1998 JP 2000519987
07-NOV-1997 US 60/064761
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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PAT
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Matches:
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Sequence 2403 from Patent WO2005019258.
CS041849 GI:61849203
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/db_xref="taxon:9606"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Compositions and methods for the treatment of imm
diseases
Patent: WO 2005016962-A 2403 24-FEB-2005;
Genentech, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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       CS032897 1116 bp DNA Sequence 2403 from Patent WO2005016962. CS032897
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BD087742 889 bp DNA linear PAT 27-AUG-2002 BMOG, novel member of myelin oligodendroglia glycoprotein family, and utilization thereof for immunomodulation.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 889)
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JP 201122389-A/2
30-NOV-201
06-NOV-1998 JP 2000519987
07-NOV-1997 US 60/064761
JEFFERY BROWNING
CI2N15/09, A61K48/00, A61F37/02, C07K14/47, C07K16/18, C07K19/00, C12N1/15,
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BMOG, novel member of myelin oligodendroglia glycoprotein family, and utilization thereof for immunomodulation
Patent: JP 2001522589-A 2 20-NOV-2001;
BIOGEN INC
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                                                                                                                                              21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer
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BD087742.1 GI:22633352
JP 2001522589-A/2.
Homo sapiens (human)
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3 (bases 1 to 1116)

Nalabolu, S.R., Raghunathan, A., Sivakamasundari, R. and Weissman, S.M. Direct Submission
Submission
Cedar Street, New Haven, CT 06510, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                           AF031136 1116 bp mRNA linear PRI 18-NOV-1997
Homo sapiens 1C7 precursor, mRNA, alternatively spliced, complete
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                                                805 CCTTCCACCAGGTCTGACAAAGGTCCAAGAAGGCAGCTGCCGGCTGCCGGC 864
745 TATTACCAGGCAAATATGCCAAATCTACTCTCCGGATTCCCCCAACTCTGAACTTTC 804
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 1116)
Nalabolu, S.R., Shukla, H., Nallur, G., Parimoo, S. and Weissman, S.M. Genes in a 220-kb region spanning the TNF cluster in human MHC Genomics 31 (2), 215-222 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="6"
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695. ,750
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                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Eutarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1613)

1 (bases 1, M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R. and Braun, A.

Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
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1.1613
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Matches:
Conservative:
Mismatches:
Indels:
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Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Email: Abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 1613.
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    BV174406
BV174406.1 GI:48009713
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                                          Homo sapiens (human)
Homo sapiens
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C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00 on novel member of myelin oligodendroglia glycoprotein CC family, and
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/organism='Homo sapiens (human)'.
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and Juji,T.
Identificastion of two novel single nucleotide polymorphisms in the NKp30 gene in human natural killer cells Unpublished
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/product."natural killer cell receptor"
/protein id="BAB78472.1"
/db_xref="GI:1721622"
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ASITVCRWBALGGGVGTGGNGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSTVAGSTV
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Homo sapiens NKp30 mRNA for natural killer cell receptor, complete
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Submitted (15-FEB-2001) Masako Sato, Japanese Red Cross Central
Blood Center, Department of Research; Hiroo4-1-31, Shibuya-ku,
Tokyo 150-0012, Japan (B-mail:masakx@cbc.jrc.or.jp,
Tel:81-3-5485-6004, Fax:81-3-3406-7892)
Location/Qualifiers
                          421 CTCCTTCGGGCTGGATTCTATGCTGTCACCTTTCTCTGTGTGCCGTGGGCAGCACCGTC
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/organism="Homo sapiens"
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Novel triggering receptor involved in natural cytotoxicity mediated
by human natural killer cells, and antibodies that identify the
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Innate Pharma S.A.S. (FR) ; Universita di
Location/Qualifiers
1. 573
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Innate Pharma S.A.S. (FR); Universita di Genova
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Moretta,A., Bottino,C. and Biassoni,R.
Movel triggering receptor involved in natural by human natural killer cells, and antibodies
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Innate Pharma S.A.S. (FR); Universita di Genova (IT)
Location/Qualifiers
1. 606
/organism="Homo sapiens"
/mol ryye="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 12 from Patent WO0136630.
AX148158
AX148158.1 GI:14347071
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1.21e-57
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Homo sapiens
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                    Percent Similarity:
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ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
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Conservative:
Mismatches:
Indels:
Gaps:
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/db_xref="taxon:9606"
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Search completed: February 28, 2006, 10:53:02 Job time : 3400 secs

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Aax59349 Human B-c

Perfect score:

Sequence:

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Scoring table:

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Ady16597 DNA encod
Aax59348 Human B-c
Add05569 Human PRO
Add05564 Human NKp
Add06564 Human Can
Adx38506 Immunomod
Aax59347 Human Can
Aax59347 Human B-c
Aax46451 Human LST
Aax464877 Human leu
Aad30466 Human NKp
Add30466 Human NKp
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Add213652 Murine can
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Aad32340 Human lun
Aad70451 DNA encod
Aac28398 DNA encod
Aav69786 Human CTL
Aav83670 Human CTL
Aas20946 DNA encod
Aas20946 DNA encod
Abz22582 Human CTL
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non-insulin dependent diabetes; allergy; immune disorder; inflammation;
cancer; neoplasm; infection; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1582
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 Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=Abss/ABSSMBs spool/VS10665259/runat_27022006_123553_27112/app_query.fasta_1
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-YGAPOP=10_-YGAPOP=10_-YGAPOP=0_S_-DELDATE_7
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Aea40217 Human nat
Adx01458 Human tol
Ady16488 DNA encod
                                                                         February 28, 2006, 06:20:29; Search time 588 Seconds (without alignments) 2278,237 Million cell updates/sec
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                                                                                                                                             1 MAWMLLLILIMVHPGSCALW......APLPPPCGSSAHLLPPVPGG 201
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         version 5.1.7
- 2006 Biocceleration Ltd.
                                                   - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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         GenCore (c) 1993
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Add89012 Adq89551 Adp95981

Human car

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AEA40217 standard;

RESULT 2 **AEA4021**  AEA40217;

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                                                                                                                                  genes involved in psychoneuroendocrinimmune (PNI) activity. The microarray is useful in diagnosing a condition associated with PNI activity, such as CFS, type-2 diabetes, allergic condition, inflammation, cancer and infection. The present sequence represents a psychoneuroendocrinimmune gene expressed sequence tag. Note the specificatio mentions SEQ ID NO of up to 3314 but only sequences up to SEQ ID NO 1829 are provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                      New microarray comprising probes for genes involved in psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a condition associated with PNI activity, e.g., inflammatory or infectious
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                                                                                                                       invention relates to a new microarray which comprises probes for
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Mismatches:
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The invention relates to isolated peptide fragments of a natural corrective fragments, analogs or derivatives, wherein the peptide fragment is ranalogs or derivatives, wherein the peptide fragment is capable of binding to a membrane-associated biomolecule of a tumor cell, and the biomolecule comprises at least one sulfated polysaccharide, and the biomolecule comprises at least one sulfated polysaccharide, and membrane-associated by NK cells, with the proviso that the peptide is other than a full length NCR polypeptide or an isolated NCR extracellular domain. Also described are: (1) an antibody that recognizes an epitope on a target membrane-associated biomolecule of a tumor cell, the biomolecule of tumor cell in a subject via an NCR-dependent mechanism; and (3) a method of cell in a subject via an NCR-dependent mechanism; and (3) a method of intentifying peptides derived from NCR which are capable of binding to a membrane-associated sulfated polysaccharide of a tumor cell. The peptide of a fragment of NCR selected from NCR4, NCB10 and NCR46. It is a fragment of the D2 domain of NCR46 comprising a sequence fully defined in the specification (SEQ ID NCS: 1 and 4). Alternatively, the peptide is a fragment of NCR46 comprising a sequence fully defined in the specification (SEQ ID NOS: 1 and 4). Alternatively, the peptide is a fragment of NCR46 comprising a sequence fully defined in the specification (SEQ ID NOS: 3 and 4). Alternatively, the peptide is a fragment of NCR46 comprising a sequence fully defined in the specification (SEQ ID NOS: 1 and 2), or a fragment of the D2 domain of NCR46 comprising a sequence fully defined in the specification (SEQ ID NOS: 3 and 4). Alternatively, the peptide is a fragment of NCR46 comprising of NCR46 composition are useful for a cell via NCR4 dependent cell line a subject via an NCR46 ependent mechanism. The regeting a tumor cell in a subject via an NCR46 ependent methods of the invention are useful for targeting to the present invention are useful for the present invention is seq
                                                                                                                                                   . cytotoxicity receptor; natural killer cell; lymphocyte; membrane; cell disintegration; antibody; hyperproliferation; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptides derived from specific natural cytotoxicity receptors and capable of binding to membrane-associated biomolecules of tumor cells, useful for targeting tumor cells to diagnose or treat benign and/or
                                                                                                         SEQ ID No:23.
                                                                                                           Human natural cytotoxicity receptor associated DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 23; 86pp; English.
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(UYNE ) UNIV BEN-GURION NEGEV RES & DEV
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The invention relates to a method of identifying a tolerance modulatory compound comprising assaying for expression or activity of at least one T regulatory (Treg) marker and at least one T effector (Teff) marker, where a change in expression or activity of the Treg marker or the Teff marker identifies the test compound as a tolerance modulatory compound. The method comprises contacting a coll with a stimulating agent and a test one Teff marker. The invention also relates to a marker and at least one Teff marker. The invention also relates to a method of identifying a tolerance promoting compound and method of identifying a tolerance modulatory compound. The method is useful for identifying a tolerance modulatory compound. The method is useful for identifying a tolerance modulatory compound. The method is useful for identifying a tolerance modulatory compound. The method is useful for compound or a tolerance modulatory compound. The methods are useful for reducing T effector cell function or for increasing T regulatory cell function or side effects of treatment with the modulator. Tolerance modulatory compounds are also useful for treating computator. Tolerance modulatory compounds are also useful for treating continument diseases, c.g. autoimmune diseases, transplant rejection or unwanted immune responses to chronically administered therapeutic proteins. Diseases include diabetes mellitus, arthritis, rheumatoid continus, sclerosis, myasthenia gravis, systemic lupus crythematosus, Hashimotos disease, dermatitis, psoriasis, ulcerative colitis, scleroderm, female genital tract inflammation, Crohns disease, sarcoidosis and pulmonary fibrosis. The compounds are further useful for enhancing immune responses, e.g. to tumors or viruses to which the body may have become tolerant. This sequence represents a human tolerance contactor.
                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a tolerance modulatory compound, useful for reducing T effector (Teff) cell function or increasing T regulatory (Treg) cell function, by assaying for expression or activity of Treg marker and Teff
                    gastrointestinal-gen.; respiratory-gen.; cytostatic; virucide; gene; ds
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                  The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
Claim 1; SEQ ID NO 2294; 158pp; English
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                                                                                                                                                                                                                                                                        CTCCTTCGGGCTGGATTCTATGCTGTCAGCTTTCTCTCTGTGGGCCGTGGGCACCGTC
                         TTCAATGCCAGCCAAGGGAGACTGGCCATTGGCTCCGTCACTGGTTCCGAGATGAGGTG
                                                                          GTTCCAGGGAAGGAGGTGAGGAATGGAACCCCAGAGTTCAGGGGCCGCCTGGCCCCACTT
                                                                                                                                  GCTTCTTCCCGTTTCCTCCATGACCACCAGGCTGAGCTGCACATCCGGGACGTGCGAGGC
                                                                                                                                                        HighepalaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly
                                                                                                                                                                      CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCTTGGTGTCGGGACAGGG
                                                                                                                                                                                                       AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu
                                                                                                                                                                                                                               AATGGGACTCGGCTGGTGGAGAAAGAACATCCTCAGCTAGGGGCTGGTACAGTCCTC
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                                                          Val ProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu
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            PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
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                                                                                                               AlaSerSerArgPheLeuHisAapHisGlnAlaGluLeuHisIleArgAspValArgGly
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    PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal
                                                        ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu
                                                                          GTTCCAGGGAAGGAAGGAATGGAACCCCAGAGTTCAG-GGGCGCCTGGCCCCACTT
                                                                                                                                           GCTTCTTCCCGTTTCCTCCATGACCACCAGGCTGAGCTGCACATCCGGGACGTGCGAGGC
                                                                                                                                                                      HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly
                                                                                                                                                                                                    CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCTTGGTGTCGGGACAGGG
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                                                                                                     Location/Qualifiers
66. .670
/*tag= a
/transl_except= (pos:291. .292, aa:Arg)
/notansl_except= (pos:291. .292, aa:Arg)
/notansl_except= the reading frame"
66. .101
/*tag= b
102. .667
/*tag= c
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                         MBOG; B-cell myelin oligodendrocyte glycoprotein; human;
Bignal transduction; immunomodulator; antiinflammatory;
autoimmune disease; inflammation; gene therapy; diagnosis;
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Human B-cell myelin oligodendrocyte glycprotein BMOG cDNA
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Matches:
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Best Local Similarity:
Query Match:
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                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                              05-NOV-1998;
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This DNA sequence encodes human BMOG, a novel member of the B cell myelin oligodendroyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene tradionuclide to a cell expressing BMOG. (All claimed)
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                        signal transduction; immunomodulator; antlinflammatory;
autoimmune disease; inflammation; gene therapy; diagnosis;
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                                                                                                                    /*tag= a /*tansl except= (pos:291. .292, aa:Arg) /note= "this codon contains an apparent 1 deletion, which alters the reading frame"
           MBOG; B-cell myelin oligodendrocyte glycoprotein; human;
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Mismatches:
Indels:
Gaps:
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                                                                                       Location/Qualifiers
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Percent Similarity:
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           The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
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Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                               The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic ansemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, polyneuropathy, This sequence represents a human PRO polynucleotide of the invention.
                                                                                                                       Claim 1; SEQ ID NO 758; 1731pp; English.
                                                                          spondyloarthropathy.
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Sequence 573 BP; 101 A; 168 C; 173 G; 130 T; 0 U; 1 Other;

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                                                                                                                                                                                                                                                                                                            181 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCCAGAGTTCAGGGGCCCCCCTGGCCCCACTT
                                                                                                                                                                                                                                                                                                                                    AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly
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          Length:
Matches:
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6 RESULT

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ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer
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                                                                                                                                                                                            Human; NXp30 receptor; natural killer cell; cytostatic; antimicrobial;
melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
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cells, comprises the amino acid sequences of the NKp30 molecule.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                 Human NKp30 receptor cDNA amplified product.
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ВЪ.
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876.00
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AAD06569 standard; cDNA; 606
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                                                                                                 (first entry)
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Best Local Similarity:
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15-NOV-1999;
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                                                AAD06569;
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AADO6569

LID AADO

XXX AADO

XXX AADO

XXX Huma

XXX Huma

XXX Hom

XXX Ho

Gaps:

US-10-696-259-6 (1-201) x AAD06569 (1-606)

Query Match:

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melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
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/product= "Human NKp30 receptor"
/nore= "The coding sequence is specifically claimed as
SEQ ID NO: 13 in claim 3"
                                                                                                                                                                    GCTTCTTCCCGTTTCCTCCATGACCACCAGGTGAGCTGCACATCCGGGACGTGCGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                  AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu
                                                                                                                                                                                                                                                                                 ATGGGACTCGGCTGGTGGAGAAAGAACATCCTCAGCTAGGGGCTGGTACAGTACTCCTC
                                                                                                                                                                                                                                  CTCCTTCGGGCTGGATTCTATGCTGTCAGCTTTCTCTCTGTGGCCGTGGGCAGCAGCACCGTC
GIGICCCAGCCCCCTGAGATICGTACCTGGAAGGATCCTCTGCCTTCCTGCCTGCTCC
                                                GITCCAGGGAAGGAAGGAGGAATGGAACCCCAGAGITCAGGGGCCGCCTGGCCCCACIT
                              PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal
                                                                                      61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu
                                                                                                                                                81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly
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/product= "Mature human NKp30 receptor"

    --GGRGTGATTCCAGAGCCCCAGATGTCCC

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HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly

101

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The invention relates to human NKp30 receptor and its corresponding cDNA molecule which is involved in natural cytotoxicity mediated by natural circle (NK) Cells and antibodies that identify the same. NKp30 receptor is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively expressed on the surface of human mature NK cells. NKp30 and its cDNA are useful for detecting and/or quantifying the presence of NK cells in a biological sample. The invention also provide kits for detecting and/or cells from a biological sample, for the selective removal of NK cells from a biological sample, for the selective removal of NK cells from a biological sample, for the selective removal of NK cells from a biological sample and for the in vitro purification of NK cells from a biological sample and for the in vitro stimulation of NK cells from a biological sample and for the in vitro stimulation of NK cells from a biological sample and for the in vitro corpuration of NK cells from a biological sample and for the in vitro stimulation of NK cells from a biological sample and for individuation of graft versus tumour (GVT) and especially graft versus leukaemia (GVL), and for the prevention, palliation and/or therapy of solid or liquid tumours, cuch as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or microorganism, notably viral infection. NKp30 antibodies are useful for dentifying NKp30 ligand expressed on an NK-susceptible target cell and the comparison of this level to the standard physiological one. Hence NKp30 controction when a necessament of the level of the recover of infection. The
                                                                                                                                                                                                                                                                                                                                              rel compound, useful for detection and/or quantifying the presence of cells, comprises the amino acid sequences of the NKp30 molecule.
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                                                                                                                                                                                                                         Biassoni R;
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 59; 83pp; English.
                       15-NOV-2000; 2000WO-EP011697.
                                                                         99CA-02288307.
                                                                                                99US-00440514.
                                                                                                                                               (INNA-) INNATE PHARMA SAS
                                                                                                                                                                                                                         Moretta A, Bottino C,
                                                                                                                                                                                                                                                                     WPI; 2001-329221/34.
P-PSDB; AAE02769.
                                                                                                                                                                       (UYGE-) UNIV GENOVA.
                                                                      15-NOV-1999;
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Sequence 674 BP; 124 A; 214 C; 183 G; 152 T; 0 U; 1 Other;

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                                                                                                                                                                     ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer
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                                                                                        MetAlaTrpMetLeuLeuLeulleLeuIleMetValHisProGlySerCysAlaLeuTrp
                                                                                                                                            ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu
                                                                                                                                                                                                                                  244 GTTCCAGGGAAGGAGGTGAATGGAACCCCAGAGTTCAGGGGCCGCCTGGCCCCACTT
                                                                                                                                                                                                                                               AlaSerSerArgPheleuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlY
Length:
Matches:
Conservative:
Mismatches:
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                 Percent Similarity:
Best Local Similarity:
Query Match:
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The present invention describes human cancer-associated (CA) nucleotide sequences (1). Also described: (1) an expression vector comprising (1); (2) a host cell comprising (1) or the expression vector; (3) a microarray for detecting a CA nucleic acid; (4) an isolated polypeptide encoded within an open reading fragment, that binds to the above polypeptide; (6) a hybridoma that produces the monoclonal antibody and a pharmaceutical composition comprising the antibody and a pharmaceutical composition comprising the antibody and a pharmaceutical composition comprising the antibody and a pharmaceutical composition comprising the antibody and a pharmaceutical composition comprising the antibody and a pharmaceutical composition comprising the antibody and a pharmaceutical composition comprising the antibody and a pharmaceutical composition comprising the antibody and a pharmaceutical composition of the polymucleotide that selectively chypridises to any of the polymucleotide sequences mentioned above; (9) methods for diagnosing cancer or for detecting the presence or absence of cancer cells in an individual; (10) a method for delivering a therapeutic agent to cancer cells in an individual; (12) an electronic library
             423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cancer-associated nucleic acid for diagnosing, preventing or treating cancer (e.g. lymphoma) or for screening agents that may be used for treating or preventing cancer.
                                                                                                                                                                                                                                  603
LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal
                                                                                                                                                                                                                      AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu
                                                                        AATGGGACTCGGCTGGTGGAGAAAGAACATCCTCAGCTAGGGGCTGGTACAGTCCTC
                                                                                                                                                           TyrTyrGlnGlyLyke------CygLeuThrTrpLysGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; cancer-associated gene; cancer-associated protein; cytostatic; gene therapy; vaccine; tyrosine kinase antagonist; G-protein coupled receptor antagonist; cancer; lymphoma; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer-associated (CA) gene sequence SEQ ID NO:28.
                                                                                                                                                                                                                                                                                           173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; SEQ ID NO 28; 143pp; English.
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comprising the polynucleotide or polypeptide, or their fragments,
mentioned above; (13) a method of screening for anticancer activity; (14)
methods for detecting cancer associated with expression of a polypeptide
correct the presence of the antibody in a test cell or serum sample; (15) a
method for screening for a bioactive agent capable of modulating the
activity of a CA protein encoded by the above nucleic acid molecule; and
(16) a method for treating cancers. (1) has cytostatic acid molecule; and
be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,
and as a G-protein coupled receptor antagonist. The compositions and
methods of the present invention can be used for diagnosing, preventing
cancer, especially lymphomas. They may also be used in
screening for agents that may be used for treating or preventing cancer.
The present sequence represents a human CA gene sequence, which is given
the exemplification of the present invention. Note: The sequence data
for this patent did not form part of the printed specification, but was
cobtained in electronic format directly from WIPO at
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3222 ATAGTGGACGGGATGGGAGGGCAGTAAGAGAGTGGGAGGAGGAGGACGACAGACCAGGA 3281
                                                                                                                                                                                                                                                                                                                                                                                                                        166
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                                                                                                                                                                                                                                                                                                                                                          3402 AGATGTCCCTAGTCCTCTTCAAAAGACCCCCAATAAATCTGCCCCACCACTAACTCCTCAT
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tragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer and a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA nucleic acid in a notation of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA nucleic acids. The antibody is useful for detecting the presence or absence of cancer cells in an individual which involves contacting cells from the individual with the antibody, where the detection of the complex correlates with the presence of cancer cells in the composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The composition is useful for inhibiting expression of a CA gene in a cell: This sequence represents human cancer-associated genomic DNA of the invariants.
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Sequence 22173 BP; 4785 A; 5863 C; 5847 G; 5678 T; 0 U; 0 Other;

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Alignment Pred. No. Score: Percent S Best Loca Query Mate	ន ៖ ដូកូ	tt Scores:: Similarity: al Similarity: .tch:	3.36e-66 52.00 52.5% 52.2% 81.7%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	22173 191 1 2 2 172 3
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ò	M	-	LeuLeulleLeulle	TrpMetLeuLeulleLeulleMetValHisProGlySer	SerCysAlaLeuTrpValSer 22
qa	2577	TGGGTCTTCCTTCTG-	  CTTCTG		ccccaggatccrgrgcrcrcrggrgtcc 2621
ò	23	-	GluileArgThrLeu	GluglySerSerAlaE	GlnProProGluileArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsn 42
qq	2622		GAGATTCGTACCCTG	GAAGGATCCTCTGCC	CAGCCCCCTGAGATTCGTACCCTGGAAGGATCCTCTGCCTTGCCTGCC
ò	43		GlyArgLeuAlalle	GlySerValThrTrpE	AlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValValPro 62
q	2682		GGGAGACTGGCCATT	GGCTCCGTCACGTGG	GCCAGCCAAGGGAGACTGGCCATTGGCTCCGTCACGTGGTTCCGAGATGAGGTGGTTCCA 2741
ò	63		WalArgAsnGlyThr	GlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAl	ArgLeuAlaProLeuAlaSer 82
අු	2742	_		CCAGAGTTCAGGGGCC	
ò	83		LeuHisAspHisGln	AlaGluLeuHisIle	SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAsp 102
q	2802		CTCCATGACCACCAG	GCTGAGCTGCACATCC	TCCCGTTTCCTCCATGACCACCAGGTGAGCTGCATCCGGGACGTGCGAGGCCATGAC 2861
ò	103	-	TyrValCysArgVal	GluValLeuGlyLeuG	AlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGlyAsnGly 122
ορ	2862		TACGTGTGCAGAGTG	GAGGTGCTGGGCCTTC	GCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCGTGTCGGGACAGGGAATGGG 2921
ò	123	-	ThrArgLeuValValGlu-Lys		129
qq	2922	-4	SGTGGTGGAGAAGGT	GAGATGCTGGGAGGTC	CTCGGCTGGTGGTGGAAAGGTGAGTGCTGGGAGGTGGTGTCTCCTCCTGGCTGG
È	129				129
q	2982		AGGCAATGTCCTTGGG	AGGCAGGGATGCTCCT	GCCCCAAGAGGCAATGTCCTTGGGAGGCAGGGATGCTCCTCTGAGGCCCCTTCCCTCCT 3041
ò	130				GluHisProGl 133
ф	3042		<b>FIGCACTICTTCCCCA</b>	ACCCCCGTCTCCATTG	GAGCCTGTGTGCACTTCTTCCCCAACCCCCGTCTCCATTGCCCCATGCAGAACATCCTCA 3101
ò	133		aGlyThrValLeuLe	nLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaValSerPh	eTyrAlaValSerPheLeuSe 153
qq	3102	-	rggtacagreerer	CCTTCGGGCTGGALTC	GCTAGGGGCTGGTACAGTCCTCCTTCGGGCTGGATTCTATGCTGTCTTCTCTCT 3161
ò	153		rvalAlavalGlySerThrValTyrT 	rTyrGlnGlyLysCys	3 166

000 313 313 314 315 315 315 315 315 315 315 315 315 315	3162 TGTGGCCGTGGGCACCGTCTATTACCAGGCAAATGTGAGTAATGGAGCCAGGGGCA 3221	166 166	3222 ATAGTGGACGGGATGGGAGGGCAGTAAGAGAGTGGGAGGAGGAGGACGACAGGACCAGGA 3281	166 166	3282 AGAGGAGAGCTCGGGACTGCAACACTGAGCAGCTCCTGTCCTCTCTGACCAGGCCAC 3341	166 166	3342 TGTCACATGGGAACACACTGCCACTCCTCAGATGGGCCCCGAGGAGTGATTCCAGAGCCC 3401	166 166	3402 AGATGTCCCTAGTCCTCTTCAAAAGACCCCAATAAATCTGCCCCACCACTAACTCCTCAT 3461	166 166	3462 GAGTCTCCAAGTGTTTTCTTCTCCATTCTCCAGATGCCAAATCTACTCTCTCCGGATTCCC 3521	167	3522 CCAACTCTGAACTTTCCCTTCCACCAGGTCTGAAAGGTCCAAGAAGGCAGCTGC 3581	177 roAlaValValProAlaProLeuProProProCysGlySerSerAlaHisLeuLeuProP 197	ליני בספלו לונים של המקור במקור במקור מינים במ	1	T 13 756 ABK84756 standard; cDNA; 81800 BP. ABK84756;	FEOUR (LIBE CHILY)	in cuna differentially expressed in granulocytic cells #1327.	in; 88; granulocytic cell; DNA chip; bacterial infection;	in intection; paragitic inflammatory disease; psoriasis;	imatoid arthritis; glomerulonephritis; asthma; thrombosis;	adula reperimina injury; renai reperimina injury; Akus; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.	sapiens.	WO200228999-A2.	11-APR-2002.	-OCT-2001; 2001WO-US030821.	-OCT-2000; 2000US-0237189P.	(GENE-) GENE LOGIC INC.	Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;	. 2002-435328/46.	Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
																	SULT 13 K84756 ABK8 ABK8		ниша	Huma	fung	rheu	card adul Croh gran	Ношо	WO20	11-A	വ	ന	(GEN	Beaz	WPI;	Dete gene mark

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30289 AGATGICCCIAGICCTCTICAAAAGACCCCCAATAAAICIGCCCCACCACTAACTCCTCAI 30348
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                                                                                                                                                                                                                                                                                                                                                                                       TGTCACATGGGAACACACTGCCACTCCTCAGATGGGCCCCGAGGAGTGATTCCAGAGCCC 30288
                                                                                                                                                                               29929 GAGCCTGTGTGCACTTCTTCCCCAACCCCGTCTCCATTGCCCCATGCAGAACATCCTCA 29988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roAlaValValProAlaProLeuProProProCysGlySerSerAlaHisLeuLeuProP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; immunosuppressive; virucide; diagnosis; prognosis; pharmaceutical; immunotherapy; cancer; cytostatic; neoplasm; autoimmune disease; immunosuppressive; immune disorder; viral infection; infection; LST-1; gene; ss.
                                            29869 GCCCCAAGAGGCAATGTCCTTGGGAGGCAGGGATGCTCCTCTGAGGCCCCTTCCCTTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LeuThrTrpLysGlyProArgArgGlnLeuP
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                       The invention relates to detecting (MI) granulocyte (GC) activation of Grane (B) (GR) identified by DNA chips analysis as given in the specification, and comparing the expression level in an unactivated GC, where captured an expression level in an unactivated GC, where captured an expression of GR is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GR; (2) screening (M3) for an agent capable of modulating GA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression or sterile inflammatory disease, by detecting the level of expression or sterile inflammatory disease, by detecting the level of expression or the gene is indicative of inflammation; (4) treating of expression in a sample of the tissue of gene(8) from GB, where the level of expression or the gene is indicative of inflammation; (4) treating of expression in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an expression in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an exposure of a subject to a pathogen or sterile inflammatory disease (e.g. for screening an agent capable of modulating GA preferably in an inflammatory disease (e.g. for screening an agent capable of modulating GA preferably in an inflammatory disease, an inflammatory disease (e.g. for screening an agent capable of modulating GA preferably in a clasue, an allergic response in a subject to a pathogen or sterile inflammatory disease, undertained injury, renal reperfusion injury, ARDS, adult correction and MS is useful for detecting an infection, parasitic infection, parasitic infection, parasitic infection, parasitic infection, parasitic infection or the p
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Matches:
Conservative:
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 SEQ ID NO 1327; 114pp; English.
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5040 CGCCTGGCCCCACTTGCTTCCCGTTTCCCTCATGACCACCAGGTGAGCTGCACATG 4981 S160 FTCCTGCCCTGCTCCTTCAATGCCAGCCAAGGGAGACTGGCCATTGGCTCCGTCACGTGG 5101 96 ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeu 115 55 75 76 ArgleuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle 95 PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp PheArgAspGluValValProGlyLysGluValArgAsnGlyThrProGluPheArgGly Sequence 6853 BP; 1798 A; 1724 C; 1832 G; 1499 T; 0 U; 0 Other; 6853 186 0 0 167 2 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-10-696-259-6 (1-201) x ADW38506 (1-6853) 3.52e-65 853.50 52.7% 52.7% 80.0% Percent Similarity: Best Local Similarity: Alignment Scores: 5100 36 26 Query Match: DB: 윱 ò ò 윱 ò g ð

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ò	129	129
QQ	4860	GGTGTCTCCTCCTGGCTGGAGGCCCCCAAGAGGCAATGTCCTTGGGAGGCAGGGATGCTCC 4801
ò	129	129
QQ	4800	TCTGAGGCCCCTTCCCTGCGTGAGCCTGTGTGCACTTCTTCCCCAACCCCCGTCTCCATT 4741
ò	130	GluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPh 146
qa	4740	GCCCCATGCAGAACATCCTCAGCTAGGGGCTGGTACAGTCCTCCTCCTTCGGGCTGGATT 4681
ò	146	eTyralaValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLyGCy 166
QQ	4680	CIATGCTGTCAGCTTTCTCTCTGTGGCCGTGGGCAGCACCGTCTATTACCAGGCGAAATG 4621
ò	166	8 166
qq	4620	  TGAGTAATGGAGCCAGGGGCAATAGTGGACGGGATGGGAGGGGGCAGTAAGAGAGTGGGAG 4561
ò	166	
đ	4560	GAGGGAGGACAGAGACCAGGAAGAGAGAGCCTCGGGACTGCAACACTGAGCAGCTCCTG 4501
ò	166	166
QQ	4500	500 TCCTCTCTCTGACCAGGCCACTGTCACATGGGAACACACTGCCACTCCTCAGATGGGCCC 4441
ò	166	166
qq	4440	CGAGGAGTGATTCCAGAGCCCAGATGTCCCTAGTCCTTTCAAAAGACCCCCAATAAATCT 4381
ò	166	166
QΩ	4380	GCCCCACCACTAACTCCTCATGAGTCTCAAGTGTTTTCTTCTCCATTCTCCAGATGCCAA 4321
ò	167	17
qq	4320	42
ò	170	ysGlybroArgArgGlnLeuProAlaValValProAlaProLeuProProProCysGlyS 190
qq	4260	AAGGICCAAGAAGGCAGCIGCCGGCTGTGCTCCCAGCGCCCCCCCCCC
ò	190	erSerAlaHisLeuLeuProProValProGlyGly 201
qq	4200	GCTCAGCACATCTGCTTCCCCCAGTCCCAGGAGGC 4166
REST AAX5 ID	934	standard; cDNA; 671 BP.
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¥ 53	20-SEP-19	99 (first entry)
\$8\$	-B III	cell myelin oligodendrocyte glycprotein BMOG cDNA.
( <u> </u>	KW MBOG; B-c KW signal tr KW autoimmun	MBOG; B-cell myelin oligodendrocyte glycoprotein; human; signal transduction; immunomodulator; antiinflammatory; autoimmune disease; inflammation; gene therapy; diagnosis; ss.
\$8\$	Homo sapie	ens.
HH	Key CDS	Location/Qualifiers 66637

305 GCTTCTTCCCGTTTCCTCCATGACCACGGCTGAGCTGCACATCCGGGACGTGCGAGGC

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This DNA sequence encodes human BMOG, a novel member of the B cell myelin oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunorequiatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG protein and eukaryotic host cells, and a method of propeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed.)
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       /traisl_except= (pos:291. .292, as:Arg)
/note= "this codon contains an apparent 1 nucleotide
deletion, which alters the reading frame"
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  120
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                               TyrTyrGlnGlyLys------CysLeuThrTrpLysGlyPro
                                                               LeuleuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal
                                                                                                         CTCCTTCGGGCTGGATTCTATGCTGTCACCTTTCTCTCTGTGGCCGTGGGCAGCACCTC
  101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly
                                                                                                                             173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
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BM36434 BS3100020
BM364361 BS3100020
BM364261 BS3100020
CB422714 604459 MA
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BQ053262 AGENCOURT
BX283861 BX283861
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BX283861 BX283863
AA846055 AK79602.8
BM088311 501749 MA
BQ0531092 AGENCOURT
CB422876 6044075 MA

AA237100 zs01h06.r AA894045 EST197848 AA236886 zs01h06.s BF522619 UI-R-C3-8

UI-R-C3-8 3497 MARC EST383603

AI511264 UAW308336 AW971514 H

CR464436 CR464436 AV599289 AV599289

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB R Maximum DB R

Searched:

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EC018752.
EC018752.1 GI:17511805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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BX773925
BE371457
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CB428376
BM917537
AA237100
                   BG744192
BG341330
BG744854
                                                                                       BG398004
BM363549
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BX283089
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BF522619
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AI511264
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AA721754
AL878396
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BQ053262
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Homo sapiens
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505
872
353
1639
471
471
379
378
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282
311
182
630
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144.5
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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BC018752
Command line parameters:
-WODEL=frame+_p2n.model -DEV=x1h
-VODEL=frame+_p2n.model -DEV=x1h
-VODEL=frame+_p2n.model -DEV=x1h
-VODEL=frame+_p2n.model -DEV=x1h
-VODELEST -OFMT=fastap -SUFFIX=p2n.rst -MINWATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-VONITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LisT=45
-VONITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LisT=45
-VOTFMT=ptc -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=USI0696259 @CGN 1 1 5315 @rumat 27022006 123556 27156 -NOFU=5 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCC118752 Homo sapi
BMS61738 ACBNCOURT
BG745027 602723117
BMS61953 AGENCOURT
BQ053062 AGENCOURT
BQ0531083 AGENCOURT
DQ052145 Homo sapi
                                                                                                                    February 28, 2006, 06:33:58 ; Search time 3876 Seconds (without alignments) 2426.265 Million cell updates/sec
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                                                                                                                                                                                                                                  1 MAWMLLLILIMVHPGSCALW.......APLPPPCGSSAHLLPPVPGG 201
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                 GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                     nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                 41078325 seqs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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BM561738
BG745027
BM561953
BQ053062
BQ053083
DQ052145
                                                                                                                                                                                                                                                                                     Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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1067
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gb_est3: *
gb_est4: *
gb_est5: *
gb_est6: *
gb_est6: *
gb_gss1: *
gb_gss2: *
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94.1
92.6
92.6
84.9
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Database

1025 1015 1004 988 988 906 876

182

Score

Result Š.

AA721754 TX82d04.8 AL878396 AL878396 DR850889 JGI\_CABE1 DN098981 JGI\_CABE8 CX747707 JGI\_ANHP6

CL037400 CH216-43D BX773925 BX773925 BE371457 601223157

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BM561738 1052 bp mRNA linear EST 20-FEB-2002
AGENCOURT 6593503 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:5484382
5', mRNA sequence.
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18 1 (bases 1 to 1052)

19 NIH-MGC http://mgc.nci.nih.gov/.

10 Unpublished (1999)

10 Contact: Robert Strausberg, Ph.D.

11 Contact: Robert Strausberg, Ph.D.

12 Contact: Robert Strausberg, Ph.D.

13 Sue Procurement: Dr. Daniel McVicar, DBS/NCI

14 Sue Procurement: Dr. Daniel McVicar, DBS/NCI

15 Consortiant Dr. Daniel McVicar, DBS/NCI

16 Consortium (LLNL)

17 Consortium (LLNL)

18 Aguencing by: Agencourt Bioscience Corporation

19 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

16 http://image.llnl.gov

17 Plate: LLCM2013 row: i column: 23

18 High quality sequence stop: 616.

18 Location/Qualifiers

18 Internation Consortium/LNL at:

19 Location/Qualifiers

10 Location/Qualifiers

10 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           709 TATTACCAGGGAAATATGCCAAATCTACTCTCCGGATTCCCCCAACTCTGAACTTTC 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   769 CCTTCCACCAGGTCTGAACCTGGAAAGGTCCAAGAAGGCAGCTGCCGGCTGTGGTCCCAGC 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
                                                                                                                                                                                                                                                                                                     CTCCTTCGGGCTGGATTCTATGCTGTCAGCTTTCTCTCTGTGGCCGTGGCCAGCAGCACCGTC
             AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly
                                   HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly
                                                                                                                           121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu
                                                                                                                                                                                                             LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                               161 TyrTyrGlnGlyLys-Cys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM561738.1 GI:18807237
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TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Heiso, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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                                                                                                                                               Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu
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Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetalaTrpMetLeuLeuLeulleLeuIleMetValHisProGlySerCysAlaLeuTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer
                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gapba-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                        human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="Blood, natural killer cell"
/clone lib="NIH MGC_106"
/lab_host="DH10B-R"
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Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4849421"
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96.1%
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Strausberg, R.
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Best Local Similarity:
Query Match:
DB:
                                                                                     12477932
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AUTHORS
TITLE
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                          TITLE
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ઠ 요 ઠે 셤 ઠે 유 ò 셤 þ

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
    CDNA Library Preparation: Ling Hong/Rubin Laboratory
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLCM1689 row: a column: 06
    High quality sequence state: 2
    High quality sequence state: 2
    High quality sequence stop: 864.
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Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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I (bases 1 to 1040)

S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabbe-rémail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Laboratory

CDNA Library Laboratory

CDNA Library Laboratory

CDNA Library Laboratory

CDNA Library Laboratory

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                                 crosccarrecricacercarearrecadareaderegraerrecageaageagereade 182
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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ArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArg
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/mol_type="mRNA"
/db_txef="taxon:9606"
/db_txef="taxon:9606"
/clone="IMAGE:5484506"
/tissue_type="natural killer cells, cell line"
/tab_hofe="blul Bobage=resistant)"
/clone_lib="NHH MGC 106"
/note="Organ: blood; Vector: pOTB7; Site_l: XhoI; Site_2:
ECORI, DNA made by oligo-dr priming. Directionally cloned
into EcoRI/Nol sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript I. RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                              841 bp mRNA linear EST 20-FEB-2002
-6593188 NIH_MGC_106 Home sapiens cDNA clone IMAGE:5484506
                                                                                                 -------LeuThrTrpLysGlyProArgArgGlnLeuProAlaValValProA 182
                                                                                                                                CCTTCCACCAGGTCTGACTGGAAAGGTCCAAAAAGGCAGCTGCCGGCTGTGGTCCCAG 177
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1 (bases 1 to 841)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMA013 row: o column: 03
High quality sequence stop: 641.
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/tissue_type="natural killer cells, cell line"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
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/note="Organ: Blood; Vector: pOTB7; Site_1: Xho1; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/Kho1 sites using the following S adaptor:
GGCACAGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superseript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                             Homindae, Homo.

Homindae, Homo.

I (bases 1 to 949)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabbe-remail.nih.gov

Tissue Procurement: Dr. Daniel Movicar, DBS/NCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboration

CLONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

RISS Location/Qualifiers

Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mismatches:
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/clone="IMAGE:5934651"
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       5', mRNA sequence.
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BQ053083.1 GI:19812423
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ECORI; CDNA made by oligo-dr priming. Directionally cloned
into EcoRI;Xho1 sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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Homo sapiens NCR3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
                                                                                                                                                   160 lTyrTyrGlnGlyLy8Cy8LeuThrTrpLy8GlyProArgArgGlnLeuProAlaValVa 180
                                                                uLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVa 160
                                                                                                                   567
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1 (Dases 1 to 573)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and
                                                                                                                                                                                                     180 lproAlaProLeuProProCys-GlySerSerAlaHisLeuLeuProProValPro 199
                                                                                                                                                                                                                               805
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Nielsen, R., Bustamante, C., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (05-MNY-2005) Celera Genomics, 45 West Gude Drive,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
                           cargacoccaecarcracererecagaeregagerecreeeccrreerereseacage
                                                     AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrVal-Le
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173
2
7
12
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Matches:
Conservative:
Mismatches:
Indels:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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DQ052145.1 GI:66905601
GSS.
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/gene="NCR3"
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876.00
90.2%
89.2%
82.1%
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Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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REFERENCE
AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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573 bp DNA linear GSS 02-JUN-2005
Pan troglodytes NCR3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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1 (bases 1 to 573)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and
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Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA sequencing genomic exons and ordering This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
61 GTGTCCCAGCCCCTGAGATTCGTACCTGGAAGGATCCTCTGCCTTCCTGCCCTGCTCC 120
                                                                                                                                           TTCAATGCCAGCCAAGGGAGACTGGCCATTGGCTCCGTCACGTGGTTCCGAGATGAGGTG 180
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pan troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                        61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
                                                                                                                                                                                                                                                                                41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal
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DQ052146.1 GI:66905602
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/clone="IMAGE:4849222"
/tissue type="natural killer cells, cell line"
/lab_host="NHOB (phage-resistant)"
/clone lib="WHH MGC 106"
/clone lib="WHH MGC 106"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, coNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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                                                          CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1688 row, h column: 23
High quality sequence stop: 802.
Location/Qualifiers
                                             DBS/NCI
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172
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21
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Matches:
Conservative:
Mismatches:
Indels:
              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar,
                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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861.50
86.3%
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DB:
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sapiens cDNA clone IMAGE:4849222 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 978)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                           US-10-696-259-6 (1-201) x DQ052146 (1-573)
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602722992F1 NIH_MGC_106 Homo
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TrpValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCys
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/clone lib="NHH MGC 48"
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Site_2: BcoRI; cDNA made by oligo-dT priming.
Directionally cloned into BcoRIXhol sites using the following 5' adaptor: GGACGAG(G). Size=eelected >500pp
for average innert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscribt II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                               BG341330 913 bp mRNA linear EST 27-FEB-2001 6024651806F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576657 5', mRNA sequence.
BG341330
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TTGATGCTCGAGGTCCCTGGCAGTTGTGGTCCTTGGCAAGTGATGTGATCCTGTGCTCTC 119
TyrTyrGlnGlyLysCysLeuThrTrpLys-----GlyProArgArgGlnLeuProAla 178
                                                                                                            -----GlySerSerAlaHis 193
                                                      TATTACCAGGCAATATGCCAAATCTACTCTCGGATTCCCCAATCTGAACTTCCCTTCC 804
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Talsaue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1289 row: 1 column: 02
High quality sequence stop: 781.
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1 (bases 1 to 913)
NAIH-MGC http://mgc.nci.nih.gov/.
Naitonal Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
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clone="IMAGE:4576657"
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BG744854 174 bp mRNA linear EST 15-MAY-2001
602722992T1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849222 3',
mRNA sequence.
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I (bases 1 to 741)

S NIH-MGC http://mgc.nci.nih.gov/.

Inth-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CON Library Preparation: Ling Hong/Rubin Laboratory

CON Library Preparation: Ling Hong/Rubin Laboratory

CON Library Preparation: Ling Hong/Rubin Laboration can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Http://image.llnl.gov

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High quality sequence stop: 741.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1689 row: a column: 06
High quality sequence stop: 719.
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1 (bases 1 to 809)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/mol_type="mRNN"
/db xref="taxon:9606"
/lab host="NBLIDB (plage-resistant)"
/lab host="NBLIDB (plage-resistant)"
/lab host="NBLIDB (plage-resistant)"
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/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector subjectionally cloned
into Ecorl/AhoI sites using the following 5' adaptor:
/GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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Fal: 217 33 598

Fax: 217 244 5617

Email: h-lewindmiuc.edu
Funding for Cattle EST sequencing was provided by the USDA National
Research Initiative, Project No. 98-35205-6644, and a grant from
Research Initiative, Project No. 98-35205-6644, and a grant from
the Japanese Ministry of Agriculture Fisheries and Forestry to
H.A.Lewin and J.E.Womack. Base-calling/Quality scores: PHRED form
Washington University Genome Center. Vector-trimming: Cross_Match
from Washington University Genome Center PHRAP suite. This sequence
is vector free and at least 200bp in length.
Insert Length: 574 Std Error: 0.00
Plate: BS320057A20 row. D column: 02
Seq primer: CGCCAAGCTCGAAATTAACCC
High quality sequence stop: 574.
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S320057A20D02 Subtracted Lewin Cattle Spleen Bos taurus cDNA clone BS320057A20D02 5', mRNA sequence.
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                                                                 100 yHisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGl 120
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I (basea I to 574)
Lewin, H.A., Soares, M.B., Pardinas, J., Liu, L. and Larson, J.H. Subtracted Lewin Cattle Spleen ESTs
Unpublished (2002)
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AUTHORS
TITLE
JOURNAL
COMMENT
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/lab_host="DH10B (phage-resistant)"
/clone lib="MIH MGC 48"
/clone lib="MIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: BCoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAGGG): Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscribt II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG398004 637 bp mRNA linear EST 12-MAR-2001 G043955121 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4565983 5',
                                       530 CATGACGCCAGCATCTACCGTGTGCACGAGTGGCAGGTGCTGGGCTTGGTGTGGGGACC 589
                                                                                                                    120 -GlyAsnGlyThrArgLeuValValGlu-LysGluHisProGlnLeuGlyAlaGly-Thr 138
                                                                                                                                                590 AGGGAATGGGATTGGTTGTTGCACGACCTGAACCTCCTCAGCTACGCGCTGCTTACA 649
                                                                                                                                                                                                                                                      Hominidae; Homo.

E 1 (bases 1 to 637)

S NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov/.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CON Library Preparation: Ling Hong/Rubin Laboration (LINL)

DNA Sequencing by: Incyt Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1283 row: o column: 08

High quality sequence stop: 628.

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                             139 ValLeuLeuLeuArg-AlaGlyPheTyrAlaValSerPheLeu-SerValAlaValGlyS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
HishspAlaSerIleTyr---ValCysArgValGluValLeuGlyLeuGlyValGlyThr
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/db xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                          GCACCGTCTATCACCAGGCCCAA 732
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BG398004.1 GI:13291452
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Pred. No.:

ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

LOCUS

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The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org
                                                                                                    Location/Qualifiers
1. .719
/organism="Homo sapiens"
                                                                                         Seq primer: Forward
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Best Local Similarity:
Query Match:
DB:
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Job time : 3882 secs
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/dev_stage="Adult"
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/clone lib="Subtracted Lewin Cattle Spleen"
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ECORI; Site_2: Xhol; This BS cDNA library was generated by
subtraction of the original non-normalized bovine spleen
bloar with 16,800 previously sequenced clones from a
bovine Placenta cDNA library. The original library was
constructed as described by Band et al (2000), Genome
Research 10(9): 1359 -1368."
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EST379519 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
AW967444
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Hegde, P., Qi.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Helt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor metagesis using a 19,200 element cDNA microarray
Contact: John Quackenbush
                                                                                                                                                                                                                                                                                                                       GCCCCAGGGATGGAGGAGTGAGACCGCAGAGTTCCAGGGCCGCTGGCCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 CCCTCTTCCCGCTTCCTCTGTGACCACGCTGAGCTGCACACATCTGGGACACCCCGAGGC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini.
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Best Local Similarity:
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AW967444
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AUTHORS
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124
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 62, Appl
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STREET: 655 Fifteenth St., NW, Suite 300, G St. Lobby
STRIE: Washington
STATE: DC
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| Sequence 1, Application US/08973544
| Patent No. 6338950
| GENERAL INFORMATION:
| APPLICANT: WEISS, Elisabeth
| TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
| NUMBER OF SEQUENCES: 4
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: TOOPY disk
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ZIP: 20005-5701
     -MODEL=frame+ p2n.model - DEV=x1h
-Q=/abss/ABSSWEB spool/US10696259/runat 27022006_123559_27221/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10696259/runat 27022006_123559_27221/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10696259/runat_27022006_123559_27221/app_query.fasta_1
-LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15
-MODE=LOCAL - OUTEMT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
-NCFU=6 - LOFU=3 - NO MAAP - NEG $CORES=0 - WAIT - DSPBLOCK=100 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THERADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 13460, A
Sequence 13461, A
Sequence 1719, Ap
Sequence 5578, Ap
Sequence 7318, Ap
Sequence 731, App
Sequence 731, App
                                                                                                                                                                     February 28, 2006, 06:56:54 ; Search time 192 Seconds (without alignments) 1860.885 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                  1 MAWMLLLILIMVHPGSCALW.....APLPPPCGSSAHLLPPVPGG 201
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                           GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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/ Cgn2 6/ptodata/1/ina/5_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/6A_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/6B_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/H_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
/ Cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
/ Cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
/ Cgn2 6/ptodata/1/ina/PP_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/PP_COMB.seq:*
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                                                                                                                          - nucleic search, using frame_plus_p2n model
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US-09-949-016-13460
US-09-949-016-13461
US-09-949-016-1718
US-09-949-016-578
US-09-03-055-1242
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Maximum Match 100%
Listing first 45 summaries
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Database :

126.5 126.5 120 120 118.5 116.5 116.5

Š. Result

Sequence 212,

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Sequence

Sequence 27, Sequence 1,

Sequence

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US-US-949-U16-11460

Sequence 13460, Application US/09949016

; Batent No. 681239

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REPERENCE: CLOOU1307

; CURRENT APPLICATION NUMBER: 60/241,755

; PRIOR APPLICATION NUMBER: 60/241,768

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-03

; PRIOR FILING DATE: 2000-10-03

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FRESEE for Windows Version 4.0

; SEQ ID NO 13460

; LEWANTH: 8100
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                                                                   3472 GCCCCATGCAGAACATCCTCAGCTAGGGGGCTGCTACAGTCCTCCT-CTTCGGGCTGGAT 3414
                                                                                                                               9413 TCTATGCTGTCAGCTTTCTCTCTGTGGCCGTGGGCAGCACCACTCTATTACCAGGCAAAT 3354
                                                                                                                                                                                                                       3353 GTGAGTAATGGAGCCAGGGCAATAGTGGACGGGATGGGAGGGGGCAGTAAGAGAGGGGA 3294
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; ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 SerCysAlaLeuTrpValSerGlnProProGluIleArgThrLeuGluGlySerSerAla 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 ArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp
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Matches:
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Gaps:
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NAME: KILE, MODICA Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 98341
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 638-5000
TELEPAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5581 DASE pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) FEATURE:
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US-08-973-544-1
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

0.0129 126.50 38.9% 29.6% 11.9%

Alignment Scores: Pred. No.: Score:	Percent Similarity: Best Local Similarity: Query Match: DB:	US-10-696-259-6 (1-201)	Oy 14 ProglySerC	Db 3724 CCTGGGTGCC	Qy 33 SerSerAlaP	Db 3784 GAAGACGCCC	3832	Qy 71 ProGluPheA	Db 3874 CCTGAGTTCT	Qy 91 AlaGluLeuH	Db 3907 GGTACGCTGA	Qy 111 GluValLeuG	Db 3967 CAGGAGGGCA	Qy 131 HisproglnL	Db 4027 TGGCCAGCC	Qy 142	Db 4087 GTGGGGATAG	Qy 150 rPheLeuSer	Db 4147 CATTCTCCTC	Qy 170 sGlyPro	Db 4204 GGGCCAGGA	Qy 186 oProCysGly	Db 4258 rctricchga	RESULT 4 US-09-949-016-1718	; Sequence 1718, Applica ; Patent No. 6812339	; GENERAL INFORMATION: ; APPLICANT: VENTER, J. ; TITLE OF INVENTION: P	; TITLE OF INVENTION:	; CURRENT APPLICATION N ; CURRENT FILING DATE:	; PRIOR APPLICATION NUM ; PRIOR FILING DATE: 20		PRIOR FILING DATE: 20
Query Match: 11.9% Indels: 50 DB: 3 Gaps: 12 US-10-696-259-6 (1-201) x US-09-949-016-13460 (1-8100)	Qy     14 ProGlySerCysAlaLeuTrpValSerGlnProProGluIleArgThrLeuGluGly 32	Qy 33 SerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySer 52	Db 3784 GAAGACGCCACTTCCAATGCCGCACAATAGCAGCAACAACGCCAAC 3831	53 ValThrTrpPheArgAspGlu	Db 3832 GTCACCTGGCGCGTCCTCCATGCCACTACACGTGGCCC 3873	Qy 71 ProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHisAapHisGln 90 1874 Crrcagartranggactorg	91 AlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrValCysArgVal	Db 3907 GGTACGCTGATCATCCAGAATGTGAACAAGAGCCATGGGGGGATATACGTGTGCCGGGTC 3966	Qy 111 GluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGlu 130	Db 3967 CAGGAGGCAACGAGTCATACCAGCAGTCCTGCGGCACCTACCT	Oy 131 HisProGlnLeuGly141 (11	Db 4027 TGGCCCACCCTACTCCCACTGTCCCGGACACTCGGTTTATCTTTGAA 4086	Qy 142AlaValSe 150	Db 4087 GTGGGGATAGAGCCAGTACCTTCAATGTGGGTTTCAAACCGGCTTGGACAGAGGGACGGA 4146	Qy 150 rPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysGysLeuThrTrpLy 170	Db 4147 CATTCTCTGCAGAGTGGGGGTCTCTGGGGGGTCTGGGGGCCTTGCAGGAGGTGGGGC 4203	Oy 170 sGlyProArgArgGlnLeuProAlaValValProAlaProLeuProPr 186	Db 4204 GGGGCCAGGAGGCTAGGGAGGCCAAGAGGGGCCACCTGAGCCATACTACC 4257	Qy 186 oProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201	Db 4258 ICCTTGCAGGCCCCCCCGGGCCCTTCCTGGACGGGAGGG 4303	RESULT 3 11S-08-949-016-11461	. 05-03-343-015-13-401 ; Sequence 13461, Application US/09949016 ; Petent No. 6812339	; GENERAL INFORMATION: ; APPLICANT: VENTER. J. Craig et al.	2.3	; FILE REFERENCE: CL001307 ; CURRENT APPLICATION NUMBER: US/09/949,016	; COKKENI FILING DAIE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/241,755 ; PRIOR FILING DATE: 2000-10-20		; PRIOR APPLICATION NUMBER: 60/231,498 ; PRIOR FILING DATE: 2000-09-08	; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0	5 557 T. D. 0. 15401 5 LENGTH: 8100 7 TYPE: DNA	; ORGANISM: Human US-09-949-016-13461

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. Craig et al.
POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                         CACTTCCAATGCCCGCACAATAGCAGCAACAAC------GCCAAC 3831
                                                                                                                                                                                                                                                                                                                                                                       | ||||::::::|||
SATCATCCAGAATGTGAACAAGAGCCATGGGGGCATATACGTGTGCCGGGTC 3966
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|GAGCCAGTACCTTCAATGTGGGTTTCAAACCGGCTTGGACAGAGGGACGGA 4146
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                                    CysAlaLeuTrpValSerGln---ProProGluIleArgThrLeuGluGly 32
                                                                                                                 PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlalleGlySer 52
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N NUMBER: US/09/949,016

E 2000-04-14

EN 2000-10-20

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NUMBER: 60/231,768

2000-10-03

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Percent Similarity:
Best Local Similarity:
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US-09-949-016-1719
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------GGCGAGGACCCCAATGGTACGCTGATCATCGAGAATGTGAACAAG 330
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                                                                                                                                                                                                                                                                                                                                                                                                                 121 AsnGlyThrArgLeuValvalGluLysGluHisProGln-------LeuGlyAla 136
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| GGCACCAAGAACCGAATCATCACAGCCGAGGGATCATCCTCCTGTTCTGCGGGGGTGGTG 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyThrVal---LeuLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAla 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   525 TCCATGTATGAGGACATCTCCCGGGGCCTCCAGGCACCTACCAGGATGTGGGCAGCTC 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             571 GGGGATGAATATGAAGATGAAAACCTTTATGAAGGC-----CTGAACCTGGACGACTGC 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LysGlyProArgArgGlnLeuProAla-- 178
                                                                                                                                                                                                                            24 ---ProProGlulleArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsn 42
                                                                                                                                                                                                                                                                                                                 GlyLysGluValArgAsnGlyThr-----ProGluPheArgGlyArgLeuAlaProLeu 80
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                                                                                                                                                                                    MetLeuleuleulleLeulleMetValHisProGlySerCysAlaLeuTrpValSerGln
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                                                                                                                                                                                                                                                                                                                                    GGC------ACTACACGTGGCCCCCTGAGTTCTTGGGCCCG-----
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                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                              US-10-696-259-6 (1-201) x US-09-949-016-1718 (1-1108)
Windows Version 4.0
                                                                                                                                             Gaps:
                                                                                    0.00354
120.00
33.9%
24.5%
11.2%
                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 SOFTWARE: FABLSEQ
                              TYPE: DNA
ORGANISM: Human
                                                    US-09-949-016-1718
          SEQ ID NO 1718
LENGTH: 1108
                                                                           Alignment Scores
                                                                                                                                                                                                                                                                         43
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US-09-949-016-1719
; Sequence 1719
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VURTER, U. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TURENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR PILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; RIOR FILING DATE: 2000-09-08
; REING APPLICATION NUMBER: 60/231,498
; RIOR FILING DATE: 2000-09-08
; REING APPLICATION NUMBER: 07/211,498
; RIOR FILING DATE: 2000-09-08
; REING APPLICATION NUMBER: 07/211,498
; RIOR FILING DATE: 2000-09-08
; REING FILING DATE: 2000-10-09-08
; REING FILING DATE: 2000-10-10-09-08
; REING FILING DATE: 2000-10-10-09-08
; REING FILING DATE: 2000-09-08
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|GCCACCAAGAACCGAATCATCACAGCCGAGGGATCATCCTCCTGTTCTGCGGGGGTGGTG 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 AGCAGCAACAACAAC-----GCCAACGTCACCTGGTGGCGCGC-----GTCCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 GlyLysGluValArgAsnGlyThr----ProGluPheArgGlyArgLeuAlaProLeu
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 122, Application US/09023655

Sequence 124, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1208
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                              133 GlnLeuGlyAlaGlyThrValLeuLeuLeuArgAla------GlyPheTyrAla 148
                                                                                                                                                                                                     149 ValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThr 168
    96 ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeu---- 113
                                                                                                                                                                                                                                                                                     669 TATAGCTITICTCCTCACAGCTGTTTCTTTGAGC-------AAAATGCTAAAG 713
                         114 ---GlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisPro
                                                                                                                                                                                                                                                                                                                           169 TrpLysGlyProArgArgGlnLeuProAlaValValProAlaProLeuProProProCys
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APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
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Matches:
Conservative:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 672 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
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LIBRARY: GENBA
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
GURRENT APPLICATION NUMBER: 02/09/949,016
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                              744
                                                                                                                        -----ValValProAlaProLeuProPr 186
                                                                                                                                                                                                     186 oProCys------ 188
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210 CTCCTGTTTTTTTTTTTCTTCATCCCTGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCT 269
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                                                                                                                                                                                                                                           745 ĠĊĊİGCTGTGCACCCAGCTCCAGTGTCTCAGCTCACTTCCCTGGGACATTCTCCTTTCAG 804
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                                                                                                                                                            685 AACATAGGAGATGTCCAGCTGGAGAAGCCGTGACACCCCTACTCCTGCCGAGGCTGCCC
                                          --LysGlyProArgArgGlnLeuProAla--
                                                                                                                                                                                                                                                                                                          805 CCCTTCTGGGGGCTTCCTTAGTCAT---ATTCCCCCAGTGGGGGGTGGG 850
                                                                                                                                                                                                                                                                                   189 ------GlySerSerAlaHisLeuLeuProProValProGlyGly 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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39.0%
27.0%
11.1%
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Best Local Similarity:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-5578
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| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVERTION: WINBER: 60/241,755
| CURRENT APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/231,768
| PRIOR PELING DATE: 2000-10-03
| PRIOR PELING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 731
| LENGTH: 672
                                                                                                   187 CCAGGCAAAGCCACTGAGGTCCGGGTGACAGTTCGGCAGGCTGACAGCCAGGTGACT 246
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                                                                                   LeuLeulleLeulleMetValHisProGlySerCys---AlaLeuTrpValSerGlnPro 24
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Sequence 31, Application US/09311784A

Patent No. 6334482

GENERAL INFORMATION:
APPLICANT: Hermanson, Gary G
APPLICANT: Batioka, Glann Y.
APPLICANT: Ishioka, Glann Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Livingston, Brian
APPLICANT: Epimmune Inc.
ITLE OF INVENTION: Immune Response and Methods of Using the Same
ITLE OF INVENTION: Immune Response and Methods of Using the STELE REFERENCE: 39963-25022.01

CURRENT APPLICATION NUMBER: US/09/311,784A

CURRENT APPLICATION NUMBER: US 60/085,751

PRIOR FILING DATE: 1999-05-15

NUMBER OF SEQ ID NOS: 463

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 31

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                        Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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; Patent No. 6852847
; GENERAL INFORMATION:
; APPLICANT: Sim, GEk.Kee
; APPLICANT: Sim, GEk.Kee
; APPLICANT: Sim, Sallins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REPREBENCE: IM-1-C1-PCT
; CURRENT APPLICATION NUMBER: 00/078,765
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR APPLICATION NUMBER: 00/078,765
; PRIOR PILING DATE: 1998-03-19
; PRIOR FILING DATE: 1998-04-17
                                                                                       700
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Matches:
Conservative:
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Indels:
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                                                                                                                                                             Gaps:
NAME/KEY: CDS
LOCATION: (1)...(681)
COTHER INFORMATION: human MB-1 Ig-alpha
US-09-311-784A-31
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Best Local Similarity:
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US-09-646-561-45/c
i Sequence 45, Application US/09646561
; Betent No. 6852847
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Sim, Gek-Ker
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; TITLE OF INVENTION: NOVEL FORMS
; FILE REFERENCE: IM-1-C1-PCT
; CURRENT APPLICATION NUMBER: 60/078,765
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
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Matches:
SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 44 LENGTH: 669
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42.7*
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US-09-646-561-44
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Best Local Similarity:
Query Match:
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537 GIGGIICIGGCCAGCAGCCGGGGTGTTGCTAGCTTCGTGTGTGTGAATATGGGTCTTCAGGC 478
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| AACGCAGCCGAGGTCCCGGTGACAGTGCT-GCGGCAGGCTGGCAGGTGACTGAAGT 419
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Patent No. 6852847
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Sellins, Karen S.
TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FLIE REFERENCE: IN-1-C1-FCT
CURRENT ELING DATE: 2000-09-19
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PRIOR APPLICATION NUMBER: 09/062,597
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 669
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PRIOR APPLICATION NUMBER: 60/078,765
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 09/062,597
PRIOR FILING DATE: 1998-04-17
NUMBER: OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 43, Application US/09646561; Patent No. 6852847; GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Selling, Karen S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang, Shumin
Sellins, Karen S.
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115.00
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                                                                                                                                      TYPE: DNA ORGANISM: Canis familiaris
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; LOCATION: (60)..(731)
US-09-646-561-41
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Best Local Similarity:
Query Match:
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US-09-646-561-43/C
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Best Local Similarity:
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        PROTEINS, NUCLEIC
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TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REPERENCE: IM-LCL-PCT.
CURRENT APPLICATION NUMBER: US/09/646,561
CURRENT FILING DATE: 2000-09-19
FRIOR APPLICATION NUMBER: 60/078,765
FRIOR PILING DATE: 1998-03-19
FRIOR PILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 43
LENGTH: 1856
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Mismatches:
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Best Local Similarity:
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Sequence 1739, Application US/10104047 Patent No. 6943241 APPLICANT: HELIX RESEARCH INSTITUTE.

US-10-104-047-1739

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PREED NO. 6882847
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Aline Shumin
APPLICANT: Aline Shumin
APPLICANT: SIM, SATEN S.
TITLE OF INVENTION: NOVEL FORMS OF I CELL COSTIMULATORY
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TITLE OF INVENTION: No. 6943241el full length cDNA; FILE REFERENCE: H1-A0105; CURRENT APPLICATION NUMBER: US/10/104,047; CURRENT FILING DATE: 2002-03-25; PRIOR APPLICATION NUMBER: PRIOR FILING DATE: NUMBER OF SEQ ID NOS: 4096; SOFTWARE: PATENTIN Ver. 2.1; SEQ ID NO 1739; LENGTH: 2220
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152 GGGTTGAGGGCCATGGACACGGGACTCTACATCTGCAAGGTGGAGGTCATGTACCCACCA 411
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                                                                                                                                                                                                                                           TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
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          FILE REFERENCE: IM-1-C1-CT-CT
CURRENT APPLICATION NUMBER: US/09/646,561
PRIOR APPLICATION NUMBER: 00/09-19
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
LENGTH: 669
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Search completed: February 28, 2006, 07:19:18 Job time : 203 secs

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    TYPE: DNA
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      Sequence 31, Appl
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Sequence 13, Appli
Sequence 13, Appl
Sequence 12, Appl
Sequence 12, Appl
                                                                                                                                                  February 28, 2006, 07:04:48; Search time 775 Seconds (without alignments) 2144.703 Million cell updates/sec
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1: /cgn2 6/ptodata1/pubpna/USO3 PUBCOMB.seq:*

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3: /cgn2 6/ptodata1/pubpna/USO3 PUBCOMB.seq:*

4: /cgn2 6/ptodata1/pubpna/USO3B_PUBCOMB.seq:*

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                       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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10 US-11-137-649-13

5 US-10-036-444-12

10 US-11-137-649-12
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                MetAlaTrpMetLeuLeuLeuIleLeuIleMetValHisProGlySerCysAlaLeuTrp
                                                    ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer
US-10-696-259-6 (1-201) x US-10-895-225A-31 (1-1061)
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ORGANISM: Homo sapien
US-10-696-259-3
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APPLICANT: BIOGEN, INC
APPLICANT: BROWNING, Jeffrey
TITLE OF INVENTION: BMOG, A Novel Protein Member of the
TITLE OF INVENTION: BMOG, A Novel Protein Member of the
TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use f
TITLE OF INVENTION: Immunomodulatory Purposes
TITLE OF INVENTION: Immunomodulatory Purposes
FILE REFERENCE: A041 US
CURRENT APPLICATION NUMBER: US/10/696,259
PRIOR APPLICATION NUMBER: US/09/560,855A
PRIOR APPLICATION NUMBER: PCT/US98/23826
PRIOR APPLICATION NUMBER: 60/664761
PRIOR APPLICATION NUMBER: 60/664761
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Length:
Matches:
Conservative:
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Indels:
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RESULT 5
US-11-137-649-13
US-11-137-649-13
Sequence 13, Application US/11137649
Publication No. US20050221438A1
GENERAL INFORMATION:
APPLICANT: UNNARE PHARMA S.A.S.
APPLICANT: UNIVERSITA DI GENOVA
TITLE OF INVERTION: "Novel triggering receptor involved in natural
TITLE OF INVENTION: Cytotoxicity mediated by human Natural Killer cells and
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 CURRENT APPLICATION NUMBER: US/10/036,444

CURRENT FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: 09/440,514

PRIOR FILING DATE: 1999-11-15

PRIOR PLICATION NUMBER: 09/456,199

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 13

LENGTH: 573
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ORGANISM: Human NK cell
US-10-036-444-13
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Publication No. US20020142445A1

GENERAL INFORMATION:

APPLICANT: INNETE PHARMA S.A.S.

APPLICANT: UNIVERSITA DI GENOVA

TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural

TITLE OF INVENTION: "A mediated by human Natural Killer cells and

TITLE OF INVENTION: antibodies that identify the same"

FILE REFERENCE: SEQ-FR-1060
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Matches:
Conservative:
Mismatches:
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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 2
; LENGTH: 889
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-696-259-2
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
TITLE OF INVENTION: antibodies that identify the FILE REFERENCE: SEQ-FR-1060
CURRENT APPLICATION NUMBER: US/11/137,649
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/036,444
PRIOR PILING DATE: 2002-01-07
PRIOR PELING DATE: 1999-11-15
PRIOR PLING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: 09/456,199
PRIOR APPLICATION NUMBER: 09/456,199
PRIOR PILING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-07
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PRIOR APPLICATION NUMBER: 09/456,199
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US-10-036-444-12
i Sequence 12, Application US/10036444
j Publication No. US20020142445A1
i GENERAL INFORMATION:
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Best Local Similarity:
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APPLICANT: UNIVERSITA DI GENOVA

ITILE OF INVENTION: "No. US20020142445Alel triggering receptor involved in natural

ITILE OF INVENTION: "No. US20020142445Alel triggering receptor involved in natural

ITILE OF INVENTION: antibodies that identify the same"

ITILE OF INVENTION: antibodies that identify the same"

FILE REFERENCE: SEQ-FR-1060

CURRENT APPLICATION NUMBER: US/10/036,444

CURRENT FILING DATE: 1999-11-07

PRIOR FILING DATE: 1999-11-07

PRIOR PLING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 12
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US-11-137-649-12
; Sequence 12, Application US/11137649
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; ORGANISM: Human NK cell
US-10-036-444-12
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Sequence 1, Application US/1003644

Publication No. US2002014245A1

GENERAL INFORMATION:
APPLICANT: INNATE PHARMA S.A.S.
APPLICANT: UNIVERSITA DI GENOVA
TITLE OF INVENTION: "No. US2002014245A1el triggering receptor involved in natural
TITLE OF INVENTION: "No. US2002014245A1el triggering receptor involved in natural
TITLE OF INVENTION: "OTCOCX.CICTY mediated by human Natural Killer cells and
TITLE OF INVENTION: antibodies that identify the same"
TITLE OF INVENTION: antibodies that identify the same"
CURRENT FILING DATE: 1090-11-15

PRIOR PELICATION NUMBER: 09/440,514

PRIOR APPLICATION NUMBER: 09/456,199

PRIOR PILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

LENGTH: 674
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ORGANISM: Human NK
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Conservative:
Mismatches:
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Publication No. US20050221438A1
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; ORGANISM: Human NK cell
US-11-137-649-12
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Best Local Similarity:
Query Match:
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                                                                                                           US-10-322-696-28

Sequence 28, Application US/10322696

Sequence 28, Application US/10322696

PUBLICANT: NO. US20040166490A1

GENERAL INFORMATION:

APPLICANT: Malandro, Marc

TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER

FILE REPERENCE: 529452001200

CURRENT APPLICATION NUMBER: US/10/322,696

CURRENT APPLICATION NUMBER: US/10/322,696

NUMBER OF SEQ ID NOS: 186

SOFTWARE: FaatSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 22173
                                             173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
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US-10-696-259-6 (1-201) x US-10-696-259-1 (1-671)	Oy 1 MetalafrpMetLeuLeulleLeulleMetValHisProGlySerCysAlaLeufrp 20	Qy 21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40	Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60	Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80	81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlV	HisaspalaSerileTyvalCysArgValGluValLeuGlyLeuGlyValGlyThrGly	Db   365 CATGACGCCAGCATCTACGTGCGAGGTGCAGGGCCTTGGTGTCGGGACAGGG 424	Oy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160 	Qy         161 TyrTyrGlnGlyLyB	Qy 173 ArgArgGlnLeuProAlaValProAlaProLeuProPro 186	RESULT 12 US-08-973-54-1/C  is Gequence 1, Application US/08973544  is bublication No. US2010010926A1  is Dublication No. US2010010926A1  is GENERAL INFORMATION:  APPLICANT: WEISS, Elisabeth  TITLE OF INVENTION:  NUMBER OF SEQUENCES: 4  CORRESPONDENCE ADDRESS:  ADDRESSEE: NITAIDO, WARMELSTEIN, MURRAY & ORAM LLP STREET: 655 Fifteenth St., NW, Suite 300, G St. Lobby CITY: Washington STATE: DC  COUNTRY: USA  ZIP: Z0005-5701  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATION SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION DATA:  APPLICATION NUMBER: PCT EP 96/02663  FILING DATE: 20-UNN-1996  PRIOR APPLICATION NUMBER: EP PS 96/02663  FILING DATE: 20-UNN-1995  FILING DATE: 20-UNN-1995
Db 3102 GCTAGGGGCTGGTACAGTCCTCCTTCGGGCTGGATTCTATGCTGTCAGCTTTCTCTC 3161	Qy     153 rValalaValGlySerThrValTyrGlnGlyLysCys       1	Qy         166	Oy 166 166  Db 3282 AGAGGAGGCTCGGGACTGCAACACTGAGCAGCTCCTGTCCTCTCTGACCAGGCCAC 3341	Oy 166 166 166 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100	166	166	Db   3462 GAGTCTCAAGTGTTTTCTTCTCCCAGATGCCAAATCTACTCTCCGGATTCCC 3521   Qy   167	Oy 177 roAlaValValProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProP 197	Qy     197 roValProGlyGly     201       Db     3642 CAGTCCCAGGAGGC     3655	RESULT 11 US-10-696-259-1 S. Sequence 1, Application US/10696259	GENERAL INFORMATION: APPLICANT: BIOGRAIN APPLICANT: BENOWING, Jeffrey APPLICANT: BENOWING, Jeffrey APPLICANT: BENOWING, Jeffrey TITLE OF INVENTION: Myella-Oligodendrocyte Glycoprotein Family and Its Use for INTELE OF INVENTION: Myella-Oligodendrocyte Glycoprotein Family and Its Use for INTELE ADAI US Immunomodulatory Purposes FILE REFERENCE: A041 US Immunomodulatory Purposes FILE REFERENCE: A041 US Immunomodulatory Purposes FILE REFERENCE: A041 US Immunomodulatory Purposes FILE REFERENCE: A041 US MYELS IS USO9/560,85A FRICA RELING DATE: 2001-04-38 FRICA PELICATION NUMBER: PCT/US98/23826 FRICA PELICATION NUMBER: FOT/US98/23826 FRICA RELING DATE: 1997-11-07 FRICA APPLICATION NUMBER: 60/664761 FRICA RELING DATE: 1997-11-07 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NUMBER: 60/664761 FRICA APPLICATION NU

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Gaquence 10, Application US/10036444

Fublication No. US20020142445A1

Gardence 10, Application US/10036444

Fublication No. US20020142445A1

GENERAL INFORMATION:

APPLICANT: INNATE PHARMA S.A.S.

APPLICANT: UNIVERSITA DI GENOVA

TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural

TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural

TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural

TITLE OF INVENTION: "No. US20020142445A1e1

FILE REFERENCE: SEQ-FR-1060

CURRENT FILING DATE: 1999-11-15

PRIOR APPLICATION NUMBER: 09/440,514

PRIOR APPLICATION NUMBER: 09/456,199

PRIOR PILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 10

LENGHAR: PatentIn Ver: 2.1

SEQ ID NO 10
                  3592 IGGIGICICCICCICCIGGCIGGAGGCCCAAGAGGAAIGICCIIGGGAGGCAGGGAIGCICC 3533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3888 TTCCTGCCCTGCTCCTTCAATGCCAAGGCAGACTGGCCATTGGCTCCGTCACGTGG 3829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3828 TTCCGAGATGAGGTGCTTCCAGGGAAGGAGGTGGAATGGAACCCCCAGAGTTCAGGGGC 3769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3652 TGGTGCGGGACAGGGAATGGGACTCGCTGGTGGTGGAGAAAGGTGAGATGCTGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 ArgAspValArgGlyHisAspAla-SerIleTyrValCysArgValGluValLeuGlyLe 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76. ArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLys----
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112201.9
FILING DATE: 03.4UG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 98341-7073
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-6110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH : 5581 base pairs
                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.29e-80
773.00
51.1%
51.1%
72.4%
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2325..2709
                                                                                                                                                                                                                                                                             TYPE: nucleic acid STRANDEDNESS: double
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1044..1162
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1475..1567
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544..652
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US-08-973-544-1
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127 40

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US-10-333-481-15

US-10-333-481-15

Sequence 15, Application US/10333481

Sequence 15, Application Work US20040072256A1

GENERAL INFORMATION:

APPLICANT: Angel Porgador

TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSI

FILE REFERENCE: 68657

CURRENT APPLICATION NUMBER: US/10/333,481

CURRENT FILING DATE: 2003-08-04

PRIOR FILING DATE: 2001-07-19

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 15

LENGTH: 405
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        MetAlaTrpMetLeuLeuLeuIleLeuIleMetValHisProGlySerCysAlaLeuTrp
                    1 MetAlaTrpMetLeuLeuLeulleLeulleMetValHisProGlySerCysAlaLeuTrp
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Matches:
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Mismatches:
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713.00
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66.8%
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ORGANISM: homo sapiens
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Best Local Similarity:
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US-10-333-481-15
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Sequence 10, Application US/11137649

Publication No. US20050221438A1

GENERAL INFORMATION:

APPLICANT: INNATE PHARMA S.A.S.

APPLICANT: UNIVERSITA DI GENOVA

TITLE OF INVENITON: "NOVEL triggering receptor involved in natural
TITLE OF INVENITON: antibodies that identify the same"

TITLE OF INVENITON: antibodies that identify the same"

TITLE OF INVENITON: antibodies that identify the same"

TITLE OF INVENITON: antibodies that identify the same"

TITLE OF INVENITON: antibodies that identify the same"

TITLE OF INVENITON: antibodies that identify the same"

TITLE OF INVENITON: antibodies that identify the same"

CURRENT APPLICATION NUMBER: US/11/137,649

PRIOR FILING DATE: 2002-01-07

PRIOR FILING DATE: 1999-11-15

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10

LENGTH: 421
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                                                                                                           ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer
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Matches:
Conservative:
Mismatches:
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ORGANISM: Human NK
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US-11-137-649-10
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Db 181 GTTCCAGGGAAGGAGGAATGGAACCCCAGAGTTCAGGGGCCGCTGGCCCCACTT 240

Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
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8 6 6 6

Search completed: February 28, 2006, 07:27:06 Job time : 786 secs

<sup>121</sup> AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGly 135

OM protein

Run on:

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or insertion/deletion polymorphism (see Tables 1
Sequence 84088, A Sequence 84184, A Sequence 84089, A Sequence 84081, A Sequence 163, App Sequence 10, Appl Sequence 10, Appl Sequence 107, App Sequence 107, App Sequence 128, Appl Sequence 107, App Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 445, Appl Sequence 45,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13510, Application US/10995561
Sequence 13510, Application US/10995561
Sequence 13510, Application No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDITOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION UNMER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13510
LENGTH: 40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45237, A
Sequence 45237, A
Sequence 397, App
Sequence 411, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 413,
Sequence 415,
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188
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US-10-276-233A-4
US-10-0623-125-439
US-11-072-512-5-439
US-10-995-561-457
US-10-995-561-457
US-10-775-169-232
US-10-750-185-45237
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US-10-750-185-45237
US-10-453-372-413
US-10-453-372-413
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US-10-453-372-415
US-10-374-954-6
US-10-374-954-6
US-10-995-561-84088
US-10-995-561-83983
US-10-995-561-84144
US-10-995-561-84089
US-10-995-561-84089
US-10-995-561-84087
US-10-821-234-163
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Matches:
Conservative:
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2 US-11-136-527-3003
US-11-072-512-1739
2 US-11-080-991-107
US-10-955-054A-50
US-10-511-538-228
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US-11-072-512-1263
2 US-11-136-527-2698
US-10-623-155-440
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US-10-453-372-409
US-11-135-855-12
US-11-135-855-13
US-11-139-499-1
US-11-000-463-484
US-11-000-463-579
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NAME/KEY: misc_feature
LOCATION: (1)...(40000)
OTHER INFORMATION: n = A,T,C or
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855.00
51.6%
    TYPE: DNA
ORGANISM: Homo sapiens
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US-10-995-561-13510/c
    US-10-995-561-13510
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   Pred. No.:
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Sequence 89, Appl
Sequence 84078, A
Sequence 84065, A
                                                                                                      February 28, 2006, 07:06:37 ; Search time 322 Seconds (without alignments) 1331.074 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
                   GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
                                                                            nucleic search, using frame_plus_p2n model
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US-10-995-561-84078
US-10-995-561-84065
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Oy 177 rohlavalvalProhlaProheuProProcyeGlySerSerAlaHisteuLeuProp 197  Db 33888 CGGCTGTGGTCCCAGGCCCCTCCCACCATGTGGAGCTCAGCATCTGCTTCCCC 33829  Oy 197 rovalProGlyQly 201  Db 33828 CAGTCCCAGGRGGC 33815  RESULT 2  US-11-12-32-89/C  Sequence 89, Application US/11122329  Publication No. US2006019272A1  Sequence 89, Application US/11122329  Publication No. US2006019272A1  APPLICANT: Geraci, Mark  APPLICANT: Geraci, Mark  APPLICANT: Geraci, Mark  APPLICANT: Oclothen, Chris  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Cells  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Cells  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene  TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene  TYPE: DIAGNOSIS SAME SAME SAME SAME SAME SAME SAME SAM	-H 0) O H 00 0) ·· I
## BOCAL Similarity: 51.4#   Mismatches: 5   172   172   172   173   174   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175	Db 34548 ACTCGCCTGGTGGAAAAGGTGAGATGCTGGGGAGGTGCTCCTCCTCGCTGGAG 34489  129

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Sequence 84065. Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDICVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: CARDICVASCULAR DISORDERS AND DRUG RESPONSE,

TITLE OF INVENTION: CARDICVASCULAR DISORDERS AND DRUG RESPONSE,

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NO 84065

LENGTH: 201
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i Sequence 84088, Application US/10995561

i Sequence 84088, Application US/10995561

i Publication No. US20050272054A1

i SEREMAL INFORMATION:

i APPLICANT: CARGILL, Michele et al.

i TITLE OF INVERTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

I TITLE OF INVERTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

I TITLE OF INVERTION: DETECTION ADD USES THEREOF

FILLE REPERENCE: CL001559

I CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SEQ ID NO 84088

LENGTH: 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 GlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrValCysArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 ValGluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLys 129
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                                                                                                                                            60 ValValProGlyLygGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaPro
GTGGAGGTGCTGGGCCTTGGTGTCGGACAGGGAATGGGACTCGGCTGGTGGTGGAAA
                                                              SerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGlu
                                                                                        139 TCCTTCAATGCCAGCCAAGGGAGACTGGCCATTGGCTCYGTCACGTGGTTCCGAGATGAG
                                                                                                                                                                                        70 ThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHis
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                 RESULT 4
US-10-995-561-84065/c
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US-10-995-561-84065
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Pred. No.:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REPERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 84078
                                                                                                                                                                                                           166
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                                                                                                                                                                                                                                                                                                                                    4560 GAGGGAGGACAGAGCCAGGAAGAGAGAGACCTCGGGACTGCAACACTGAGCAGCTCCTG 4501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4320 ATCTACTCTCTCCGGATTCCCCCAACTCTGAACTTTCCCTTCCACCAGGTCTGACCTGGA 4261
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                                      4800 TCTGAGGCCCCTTCCCTTGAGCCTGTGTGCACTTCTTCCCCAACCCCCGTCTCCATT
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Matches:
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... Sequence 84078, Application US/10995561
... Publication No. US/0050272054A1
... GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-995-561-84078
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US-10-995-561-84089/c

US-10-995-561-84089/c

Sequence 84089, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
TITLE OF INVENTION: GENERAL SECURATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOUTHARD FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SEQ ID NO 84089

LENGTH: 201

MANDER OF SEQ ID WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                  150 SerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLygCygLeuThrTrp 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 LeuThrTrpLysGlyProArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 84082, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
    APPLICANT: CARGILL, Michele et al.
    TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
    TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS ITILE OF INVENTION: DETECTION AND USES THEREOF
    FILE REFERENCE: CL001559
                                                                                                                                                                                                                                                                                                                       130 GluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaVal
                                                                                                                                                                                                                                                                                                                                                  76 AGCTITCTCTCTGTGGCCGTGGGCACCACTCTATTACCAGGGCAATGTGAGTAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 CTGACCTGGAAAGGTCCAAGAAGKCAGCTGCCGGCTGTGGTCCCCAGCGCCCCCCCCCACCA
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 84144; LENGTH: 201; TYPE: DNO TYPE: DNO Sapiens US-10-995-561-84144
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Pred. No.:
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US-10-995-561-83983/c
| Sequence 83983, Application US/10995561
| Publication No. US20050272054A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al.
| TITLE OF INVENTION: CREDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, TITLE OF INVENTION: DETECTION AND USES THEREOF
| TITLE OF INVENTION: DETECTION AND USES THEREOF
| TITLE OF INVENTION: DATE: 1004-11-24
| CURRENT APPLICATION NUMBER: US/10/995,561
| CURRENT FILING DATE: 2004-11-24
| NUMBER OF SEQ ID NOS: 85702
| SEQ ID NO 83983
| LENGTH: 201
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US-10-995-561-84144/C
US-10-995-561-84144/C
; Sequence 84144, Application US/10995561
; Sequence 84144, Application US/20050272054A1
; GENERAL INPORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFRENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
                                                                                                                                                                                                                                                              167 LeuThrTrpLysGlyProArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
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                                                                                                                                                                                                                                                                                   187 ProCysGlySerSerAlaHisLeuLeuProProValBroGlyGly 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 CysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
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Indels:
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                                                                                                                                                                                       Gaps:
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ORGANISM: Homo sapiens
                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
 ; TYPE: DNA
; ORGANISM: HOMO E
US-10-995-561-84088
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US-10-995-561-83983
                                                                        Alignment Scores:
Pred. No.:
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Pred. No.:
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DB:
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APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEQ IN NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 163
LENGTH: 2754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||||||:::|||||||||||:::||||:::
296 GCCTGGCTGCTGCTGCTGCTGCTGCATCATTACAGGCCGGTGCCCGCGGGGTGAG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
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233
433
992
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Matches:
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Indels:
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            Publication No. US20050255114A1
GENERAL INFORMATION:
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122.00
37.2%
26.5%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL,
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDICOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILLING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOCTHARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 84087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 GluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaVal 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 SerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLy8Cy8LeuThrTrp 169
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Matches:
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CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SECTYARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84082
LENGTH: 201
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                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-995-561-84082
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CORGANISM: Homo sapiens
US-10-995-561-84087
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Best Local Similarity:
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| | | | ::: ::: CCTGGGACGCTGTTCAGGAAACGATGGCAGAACGAGAAGCTTGGATGCC 570
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3003, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION Brobe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 GATGACCCCTTCTGCAGTGCTACCTTT---AATGAAAGCAGAGTGAACCTCACCATCCAA 351
                                                                                                                                           625 TCCATGTATGAGGACATCTCCCGGGGCCTCCAGGGCACCTACCAGGATGTGGGCAGCTC
                                                                  571 GGGGATGAATATGAAGATGAAAACCTTTATGAAGGC-----CTGAACCTGGACGACTGC
                                                                                                                ----LysGlyProArgArgGlnLeuProAla--
                                                                                                                                                                                 ----ValValProAlaProLeuProPr
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                                                                                                                                                                                                                                                                                                                                       805 CCCTTCTGGGGGCTTCCTTAGTCAT---ATTCCCCCAGTGGGGGGGGG 850
                                            ------GlySerSerAlaHisLeuLeuProProValProGlyGly
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; ORGANISM: Rattus
US-11-136-527-3003
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                                                                              APPLICANT: BERTUCCI, Francois
APPLICANT: BERTUCCI, Francois
APPLICANT: BERTUCCI, Remi
APPLICANT: HOULGATTE, Remi
TITLE OF INNENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
FILE REFERENCE: 1423-R-03
CURRENT APPLICATION NUMBER: US 60/525,987
PRIOR FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: US 60/525,987
NUMBER OF SEQ ID NOS: 1596
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 1107
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 GTCCCAGCATCATTGATGGTGAGCCTGGGGAAGACGCCCACTTCCAATGCCCGCACAAT 207
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OTHER INFORMATION: Description of Artificial sequences:primer
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1107)
OTHER INFORMATION: cd79a antigen (immunoglobulin-associated
OTHER INFORMATION: alpha) (CD79A) gene.
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Indels:
Gaps:
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                              Sequence 10, Application US/11000688 Publication No. US20050287544A1 GENERAL INFORMATION:
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Best Local Similarity:
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Squence 107, Application US/11080991

Squence 107, Application US/11080991

Squence 107, Application VGS005066437A1

GENERAL INFORMATION:

APPLICANT: Veiby, Petter Ole

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: AND OVARIAN CANCER

TITLE OF INVENTION: AND OVARIAN CANCER

TITLE OF INVENTION: AND OVARIAN CANCER

TITLE OF INTENTION: AND OVARIAN CANCER

TITLE OF INTENTION NUMBER: US/11/080,991

CURRENT FILING DATE: 2005-03-11

PRIOR PELING DATE: 2002-06-21

NUMBER OF SEQ ID NOS: 112

SOUTHARD: FESTERE OF Windows Version 4.0

SEQ ID NO 107

LENGTH: 2467
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1067 CTTCGCTGTGCAGCCCGGGGCAGCCCCTCGCATTGGCTGGACTGTCAACGACCGG 1126
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                      88 AspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrVal 107
28 ArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArg
                                                                                                                                                                                                                                                                             108 CysArgValGlu---ValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuVal
                                                                                                                                                                                                                                                                                                                                                                             48 LeuAlaIleGlySerValThrTrpPheArgAspGluValValProGlyLysGluValArg
                                                                                                                                        68 AsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHis
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LOCATION: 2453, 2454, 2455, 2456,
LOCATION: 2453, 2464, 2465, 2466,
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-11-080-991-107
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US-11-080-991-107
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                                                                                                                                                            150 SerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLy8CysLeuThrTrp 169
                                                                                                                                                                                                                                             532 AGTTTCCTGGTCACCGCTGTTTCTTTGAACAGGACGSTARWGWAAAGAAGTCCTCTTACA 591
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97 AspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeu-
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APPLICANT: MASUHO, YASUHIKO
TITLE OP INVENTION: NOVEL [411] length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR PILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
NUMBER OF SEQ ID NOS: 4096
NUMBER OF SEQ ID NOS: 4096
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAMA, TSUTOMU
OTSUKA, MOTOYUKI
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US-11-072-512-1739
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